

SEQUENCE LISTING

<110> Han, Hui-Quan
Kwak, Keith

<120> Human E3 Alpha Ubiquitin Ligase

<130> 01017/35966

<140>

<141>

<150> US 60/187,911

<151> 1999-03-08

<160> 29

<170> PatentIn Ver. 2.0

<210> 1

<211> 6308

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (696)..(5942)

<400> 1

gccaagaatt cggcacgagg ggaaaagctg agccaggaa ccaaattact tgctttacct 60
cattgtgtaa gacaagcgtc aaaaacagct tcaacctatc ttgaacaaga gaacttacct 120
ccaaaggctt atcatctgtc ttccacttat ccaacaagct gctatggcca ctgctgtgct 180
cgcacctgga accaccgcca gcccactac tgctccact accactgggt ctcccacct 240
gatcagctgc ttgctgtgct catcttatcc gcttctgctt gttctgagta aatgtataca 300
caccctggaa accaccattc tactttctgt gtctatgaat ttgactactc tagctggatc 360
ccgagctttt ttgtacacat gtgcaagtgc ccacggggta gaatcctaaa aatagaagat 420
gtatgcaaca gttcccagca ccaaacccag atatacaacc attcagctac caagagctac 480
gcctgataaa ttagagggga aaaaaaaaaat ctccagtcct ttcacgtcgt gacgcttgct 540
tccgggaagc gggccggaag ccactcctcg agtctgcgtc aaaccgact tcaggggccc 600
tcgtaaaagt gtcgtccctg tctctccgac cgccacagg ttccgcttg cctctggccc 660
ggggtcggca actgcaggcg tcagtttccc tcaag atg gcg gac gag gag gct 713
Met Ala Asp Glu Glu Ala
1 5
gga ggt act gag agg atg gaa atc agc gcg gag tta ccc cag acc cct 761
Gly Gly Thr Glu Arg Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro
10 15 20
cag cgt ctg gca tct tgg tgg gat cag caa gtt gat ttt tat act gct 809
Gln Arg Leu Ala Ser Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala
25 30 35

ttc Phe	ttg Leu 40	cat His	cat His	ttg Leu	gca Ala	caa Gln 45	ttg Leu	gtg Val	cca Pro	gaa Glu	att Ile 50	tac Tyr	ttt Phe	gct Ala	gaa Glu	857
atg Met 55	gac Asp	cca Pro	gac Asp	ttg Leu	gaa Glu 60	aag Lys	cag Gln	gag Glu	gaa Glu	agt Ser 65	gta Val	caa Gln	atg Met	tca Ser	ata Ile 70	905
ttc Phe	act Thr	cca Pro	ctg Leu	gaa Glu 75	tgg Trp	tac Tyr	tta Leu	ttt Phe	gga Gly 80	gaa Glu	gat Asp	cca Pro	gat Asp	att Ile 85	tgc Cys	953
tta Leu	gag Glu	aaa Lys	ttg Leu 90	aag Lys	cac His	agt Ser	gga Gly	gca Ala 95	ttt Phe	cag Gln	ctt Leu	tgt Cys	ggg Gly 100	agg Arg	gtt Val	1001
ttc Phe	aaa Lys	agt Ser 105	gga Gly	gag Glu	aca Thr	acc Thr	tat Tyr 110	tct Ser	tgc Cys	agg Arg	gat Asp	tgt Cys 115	gca Ala	att Ile	gat Asp	1049
cca Pro	aca Thr 120	tgt Cys	gta Val	ctc Leu	tgt Cys	atg Met 125	gac Asp	tgc Cys	ttc Phe	cag Gln	gac Asp 130	agt Ser	gtt Val	cat His	aaa Lys	1097
aat Asn 135	cat His	cgt Arg	tac Tyr	aag Lys	atg Met 140	cat His	act Thr	tct Ser	act Thr	gga Gly 145	gga Gly	ggg Gly	ttc Phe	tgt Cys	gac Asp 150	1145
tgt Cys	gga Gly	gac Asp	aca Thr	gag Glu 155	gca Ala	tgg Trp	aaa Lys	act Thr	ggc Gly 160	cct Pro	ttt Phe	tgt Cys	gta Val	aat Asn 165	cat His	1193
gaa Glu	cct Pro	gga Gly	aga Arg 170	gca Ala	ggc Gly	act Thr	ata Ile	aaa Lys 175	gag Glu	aat Asn	tca Ser	cgc Arg	tgt Cys 180	ccg Pro	ttg Leu	1241
aat Asn	gaa Glu	gag Glu 185	gta Val	att Ile	gtc Val	caa Gln	gcc Ala 190	agg Arg	aaa Lys	ata Ile	ttt Phe	cct Pro 195	tca Ser	gtg Val	ata Ile	1289
aaa Lys	tat Tyr 200	gtc Val	gta Val	gaa Glu	atg Met	act Thr 205	ata Ile	tgg Trp	gaa Glu	gag Glu	gaa Glu 210	aaa Lys	gaa Glu	ctg Leu	cct Pro	1337
cct Pro 215	gaa Glu	ctc Leu	cag Gln	ata Ile	agg Arg 220	gag Glu	aaa Lys	aat Asn	gaa Glu	aga Arg 225	tac Tyr	tat Tyr	tgt Cys	gtc Val	ctt Leu 230	1385
ttc Phe	aat Asn	gat Asp	gaa Glu	cac His 235	cat His	tca Ser	tat Tyr	gac Asp	cac His 240	gtc Val	ata Ile	tac Tyr	agc Ser	cta Leu 245	caa Gln	1433
aga Arg	gct Ala	ctt Leu	gac Asp 250	tgt Cys	gag Glu	ctc Leu	gca Ala	gag Glu 255	gcc Ala	cag Gln	ttg Leu	cat His	acc Thr 260	act Thr	gcc Ala	1481
att Ile	gac Asp	aaa Lys 265	gag Glu	ggc Gly	cgt Arg	cgg Arg	gct Ala 270	gtt Val	aaa Lys	gcg Ala	gga Gly 275	gct Ala	tat Tyr	gct Ala	gct Ala	1529
tgc Cys	cag Gln 280	gaa Glu	gca Ala	aag Lys	gaa Glu	gat Asp 285	ata Ile	aag Lys	agt Ser	cat His	tca Ser 290	gaa Glu	aat Asn	gtc Val	tct Ser	1577

caa Gln 295	cat His	cca Pro	ctt Leu	cat His	gta Val 300	gaa Glu	gta Val	tta Leu	cac His	tca Ser 305	gag Glu	att Ile	atg Met	gct Ala	cat His 310	1625
cag Gln	aaa Lys	ttt Phe	gct Ala	ttg Leu 315	cgt Arg	ctt Leu	ggg Gly	tcc Ser	tgg Trp 320	atg Met	aac Asn	aaa Lys	att Ile	atg Met 325	agc Ser	1673
tat Tyr	tca Ser	agt Ser	gac Asp 330	ttt Phe	agg Arg	cag Gln	atc Ile	ttt Phe 335	tgc Cys	caa Gln	gca Ala	tgc Cys	ctt Leu 340	aga Arg	gaa Glu	1721
gaa Glu	cct Pro	gac Asp 345	tcg Ser	gag Glu	aat Asn	ccc Pro	tgt Cys 350	ctc Leu	ata Ile	agc Ser	agg Arg	tta Leu 355	atg Met	ctt Leu	tgg Trp	1769
gat Asp	gca Ala 360	aag Lys	ctt Leu	tat Tyr	aaa Lys	ggg Gly 365	gcc Ala	cgt Arg	aag Lys	atc Ile	ctt Leu 370	cat His	gaa Glu	ttg Leu	atc Ile	1817
ttc Phe 375	agc Ser	agt Ser	ttt Phe	ttt Phe	atg Met 380	gag Glu	atg Met	gaa Glu	tac Tyr	aaa Lys 385	aaa Lys	ctc Leu	ttt Phe	gct Ala	atg Met 390	1865
gaa Glu	ttt Phe	gtg Val	aag Lys	tat Tyr 395	tat Tyr	aaa Lys	caa Gln	ctg Leu	cag Gln 400	aaa Lys	gaa Glu	tat Tyr	atc Ile	agt Ser 405	gat Asp	1913
gat Asp	cat His	gac Asp 410	aga Arg	agt Ser	atc Ile	tct Ser	ata Ile	act Thr 415	gca Ala	ctt Leu	tca Ser	gtt Val	cag Gln 420	atg Met	ttt Phe	1961
act Thr	gtt Val	cct Pro 425	act Thr	ctg Leu	gct Ala	cga Arg	cat His 430	ctt Leu	att Ile	gaa Glu	gag Glu	cag Gln 435	aat Asn	gtt Val	atc Ile	2009
tct Ser	gtc Val 440	att Ile	act Thr	gaa Glu	act Thr	ctg Leu 445	cta Leu	gaa Glu	gtt Val	tta Leu	cct Pro 450	gag Glu	tac Tyr	ttg Leu	gac Asp	2057
agg Arg 455	aac Asn	aat Asn	aaa Lys	ttc Phe	aac Asn 460	ttc Phe	cag Gln	ggg Gly	tat Tyr	agc Ser 465	cag Gln	gac Asp	aaa Lys	ttg Leu	gga Gly 470	2105
aga Arg	gta Val	tat Tyr	gca Ala	gta Val 475	ata Ile	tgt Cys	gac Asp	cta Leu	aag Lys 480	tat Tyr	atc Ile	ctg Leu	atc Ile	agc Ser 485	aaa Lys	2153
ccc Pro	aca Thr	ata Ile	tgg Trp 490	aca Thr	gaa Glu	aga Arg	tta Leu	aga Arg 495	atg Met	cag Gln	ttc Phe	ctt Leu	gaa Glu 500	ggg Gly	ttt Phe	2201
cga Arg	tct Ser	ttt Phe 505	ttg Leu	aag Lys	att Ile	ctt Leu	acc Thr 510	tgt Cys	atg Met	cag Gln	gga Gly	atg Met 515	gaa Glu	gaa Glu	atc Ile	2249
cga Arg	aga Arg 520	cag Gln	gtt Val	ggg Gly	caa Gln	cac His 525	att Ile	gaa Glu	gtg Val	gat Asp	cct Pro 530	gat Asp	tgg Trp	gag Glu	gct Ala	2297
gcc Ala 535	att Ile	gct Ala	ata Ile	cag Gln 540	atg Met	caa Gln	ttg Leu	aag Lys	aat Asn	att Ile 545	tta Leu	ctc Leu	atg Met	ttc Phe	caa Gln 550	2345

gag	tgg	tgt	gct	tgt	gat	gaa	gaa	ctc	tta	ctt	gtg	gct	tat	aaa	gaa	2393
Glu	Trp	Cys	Ala	Cys	Asp	Glu	Glu	Leu	Leu	Leu	Val	Ala	Tyr	Lys	Glu	
			555						560					565		
tgt	cac	aaa	gct	gtg	atg	agg	tgc	agt	acc	agt	ttc	ata	tct	agt	agc	2441
Cys	His	Lys	Ala	Val	Met	Arg	Cys	Ser	Thr	Ser	Phe	Ile	Ser	Ser	Ser	
			570					575					580			
aag	aca	gta	gta	caa	tcg	tgt	gga	cat	agt	ttg	gaa	aca	aag	tcc	tac	2489
Lys	Thr	Val	Val	Gln	Ser	Cys	Gly	His	Ser	Leu	Glu	Thr	Lys	Ser	Tyr	
		585					590					595				
aga	gta	tct	gag	gat	ctt	gta	agc	ata	cat	ctg	cca	ctc	tct	agg	acc	2537
Arg	Val	Ser	Glu	Asp	Leu	Val	Ser	Ile	His	Leu	Pro	Leu	Ser	Arg	Thr	
	600					605					610					
ctt	gct	ggg	ctt	cat	gta	cgt	tta	agc	agg	ctg	ggg	gct	gtt	tca	aga	2585
Leu	Ala	Gly	Leu	His	Val	Arg	Leu	Ser	Arg	Leu	Gly	Ala	Val	Ser	Arg	
	615				620					625					630	
ctg	cat	gaa	ttt	gtg	tct	ttt	gag	gac	ttt	caa	gta	gag	gta	cta	gtg	2633
Leu	His	Glu	Phe	Val	Ser	Phe	Glu	Asp	Phe	Gln	Val	Glu	Val	Leu	Val	
				635					640					645		
gaa	tat	cct	tta	cgt	tgt	ctg	gtg	ttg	gtt	gcc	cag	gtt	gtt	gct	gag	2681
Glu	Tyr	Pro	Leu	Arg	Cys	Leu	Val	Leu	Val	Ala	Gln	Val	Val	Ala	Glu	
			650					655					660			
atg	tgg	cga	aga	aat	gga	ctg	tct	ctt	att	agc	cag	gtg	ttt	tat	tac	2729
Met	Trp	Arg	Arg	Asn	Gly	Leu	Ser	Leu	Ile	Ser	Gln	Val	Phe	Tyr	Tyr	
			665				670					675				
caa	gat	gtt	aag	tgc	aga	gaa	gaa	atg	tat	gat	aaa	gat	atc	atc	atg	2777
Gln	Asp	Val	Lys	Cys	Arg	Glu	Glu	Met	Tyr	Asp	Lys	Asp	Ile	Ile	Met	
	680					685					690					
ctt	cag	att	ggg	gca	tct	tta	atg	gat	ccc	aat	aag	ttc	ttg	tta	ctg	2825
Leu	Gln	Ile	Gly	Ala	Ser	Leu	Met	Asp	Pro	Asn	Lys	Phe	Leu	Leu	Leu	
	695				700					705					710	
gta	ctt	cag	agg	tat	gaa	ctt	gcc	gag	gct	ttt	aac	aag	acc	ata	tct	2873
Val	Leu	Gln	Arg	Tyr	Glu	Leu	Ala	Glu	Ala	Phe	Asn	Lys	Thr	Ile	Ser	
				715					720					725		
aca	aaa	gac	cag	gat	ttg	att	aaa	caa	tat	aat	aca	cta	ata	gaa	gaa	2921
Thr	Lys	Asp	Gln	Asp	Leu	Ile	Lys	Gln	Tyr	Asn	Thr	Leu	Ile	Glu	Glu	
			730					735					740			
atg	ctt	cag	gtc	ctc	atc	tat	att	gtg	ggg	gag	cgt	tat	gta	cct	gga	2969
Met	Leu	Gln	Val	Leu	Ile	Tyr	Ile	Val	Gly	Glu	Arg	Tyr	Val	Pro	Gly	
			745				750					755				
gtg	gga	aat	gtg	acc	aaa	gaa	gag	gtc	aca	atg	aga	gaa	atc	att	cac	3017
Val	Gly	Asn	Val	Thr	Lys	Glu	Glu	Val	Thr	Met	Arg	Glu	Ile	Ile	His	
	760					765					770					
ttg	ctt	tgc	att	gaa	ccc	atg	cca	cac	agt	gcc	att	gcc	aaa	aat	tta	3065
Leu	Leu	Cys	Ile	Glu	Pro	Met	Pro	His	Ser	Ala	Ile	Ala	Lys	Asn	Leu	
	775				780					785					790	
cct	gag	aat	gaa	aat	aat	gaa	act	ggc	tta	gag	aat	gtc	ata	aac	aaa	3113
Pro	Glu	Asn	Glu	Asn	Asn	Glu	Thr	Gly	Leu	Glu	Asn	Val	Ile	Asn	Lys	
				795					800					805		

gtg gcc aca ttt aag aaa cca ggt gta tca ggc cat gga gtt tat gaa	3161
Val Ala Thr Phe Lys Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu	
810 815 820	
cta aaa gat gaa tca ctg aaa gac ttc aat atg tac ttt tat cat tac	3209
Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr	
825 830 835	
tcc aaa acc cag cat agc aag gct gaa cat atg cag aag aaa agg aga	3257
Ser Lys Thr Gln His Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg	
840 845 850	
aaa caa gaa aac aaa gat gaa gca ttg ccg cca cca cca cct cct gaa	3305
Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro Pro Pro Pro Pro Pro Glu	
855 860 865 870	
ttc tgc cct gct ttc agc aaa gtg att aac ctt ctc aac tgt gat atc	3353
Phe Cys Pro Ala Phe Ser Lys Val Ile Asn Leu Leu Asn Cys Asp Ile	
875 880 885	
atg atg tac att ctc agg acc gta ttt gag cgg gca ata gac aca gat	3401
Met Met Tyr Ile Leu Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp	
890 895 900	
tct aac ttg tgg acc gaa ggg atg ctc caa atg gct ttt cat att ctg	3449
Ser Asn Leu Trp Thr Glu Gly Met Leu Gln Met Ala Phe His Ile Leu	
905 910 915	
gca ttg ggt tta cta gaa gag aag caa cag ctt caa aaa gct cct gaa	3497
Ala Leu Gly Leu Leu Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu	
920 925 930	
gaa gaa gta aca ttt gac ttt tat cat aag gct tca aga ttg gga agt	3545
Glu Glu Val Thr Phe Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser	
935 940 945 950	
tca gcc atg aat ata caa atg ctt ttg gaa aaa ctc aaa gga att ccc	3593
Ser Ala Met Asn Ile Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro	
955 960 965	
cag tta gaa ggc cag aag gac atg ata acg tgg ata ctt cag atg ttt	3641
Gln Leu Glu Gly Gln Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe	
970 975 980	
gac aca gtg aag cga tta aga gaa aaa tct tgt tta att gta gca acc	3689
Asp Thr Val Lys Arg Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr	
985 990 995	
aca tca gga tcg gaa tct att aag aat gat gag att act cat gat aaa	3737
Thr Ser Gly Ser Glu Ser Ile Lys Asn Asp Glu Ile Thr His Asp Lys	
1000 1005 1010	
gaa aaa gca gaa cga aaa aga aaa gct gaa gct gct agg cta cat cgc	3785
Glu Lys Ala Glu Arg Lys Arg Lys Ala Glu Ala Ala Arg Leu His Arg	
1015 1020 1025 1030	
cag aag atc atg gct cag atg tct gcc tta cag aaa aac ttc att gaa	3833
Gln Lys Ile Met Ala Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu	
1035 1040 1045	
act cat aaa ctc atg tat gac aat aca tca gaa atg cct ggg aaa gaa	3881
Thr His Lys Leu Met Tyr Asp Asn Thr Ser Glu Met Pro Gly Lys Glu	
1050 1055 1060	

gat Asp	tcc Ser	att Ile	atg Met	gag Glu	gaa Glu	gag Glu	agc Ser	acc Thr	cca Pro	gca Ala	gtc Val	agt Ser	gac Asp	tac Tyr	tct Ser	3929	
1065			1070						1075								
aga Arg	att Ile	gct Ala	ttg Leu	ggt Gly	cct Pro	aaa Lys	cgg Arg	ggt Gly	cca Pro	tct Ser	gtt Val	act Thr	gaa Glu	aag Lys	gag Glu	3977	
1080			1085						1090								
gtg Val	ctg Leu	acg Thr	tgc Cys	atc Ile	ctt Leu	tgc Cys	caa Gln	gaa Glu	gaa Glu	cag Gln	gag Glu	gtg Val	aaa Lys	ata Ile	gaa Glu	4025	
1095			1100						1105						1110		
aat Asn	aat Asn	gcc Ala	atg Met	gta Val	tta Leu	tcg Ser	gcc Ala	tgt Cys	gtc Val	cag Gln	aaa Lys	tct Ser	act Thr	gcc Ala	tta Leu	4073	
			1115						1120						1125		
acc Thr	cag Gln	cac His	agg Arg	gga Gly	aaa Lys	ccc Pro	ata Ile	gaa Glu	ctc Leu	tca Ser	gga Gly	gaa Glu	gcc Ala	cta Leu	gac Asp	4121	
			1130						1135						1140		
cca Pro	ctt Leu	ttc Phe	atg Met	gat Asp	cca Pro	gac Asp	ttg Leu	gca Ala	tat Tyr	gga Gly	act Thr	tat Tyr	aca Thr	gga Gly	agc Ser	4169	
1145			1150						1155								
tgt Cys	ggt Gly	cat His	gta Val	atg Met	cac His	gca Ala	gtg Val	tgc Cys	tgg Trp	cag Gln	aag Lys	tat Tyr	ttt Phe	gaa Glu	gct Ala	4217	
1160			1165						1170								
gta Val	cag Gln	ctg Leu	agc Ser	tct Ser	cag Gln	cag Gln	cgc Arg	att Ile	cat His	gtt Val	gac Asp	ctt Leu	ttt Phe	gac Asp	ttg Leu	4265	
1175			1180						1185						1190		
gaa Glu	agt Ser	gga Gly	gaa Glu	tat Tyr	ctt Leu	tgc Cys	cct Pro	ctt Leu	tgc Cys	aaa Lys	tct Ser	ctg Leu	tgc Cys	aat Asn	act Thr	4313	
			1195						1200						1205		
gtg Val	atc Ile	ccc Pro	att Ile	att Ile	cct Pro	ttg Leu	caa Gln	cct Pro	caa Gln	aag Lys	ata Ile	aac Asn	agt Ser	gag Glu	aat Asn	4361	
1210			1215						1220								
gca Ala	gat Asp	gct Ala	ctt Leu	gct Ala	caa Gln	ctt Leu	ttg Leu	acc Thr	ctg Leu	gca Ala	cgg Arg	tgg Trp	ata Ile	cag Gln	act Thr	4409	
1225			1230						1235								
gtt Val	ctg Leu	gcc Ala	aga Arg	ata Ile	tca Ser	ggt Gly	tat Tyr	aat Asn	ata Ile	aga Arg	cat His	gct Ala	aaa Lys	gga Gly	gaa Glu	4457	
1240			1245						1250								
aac Asn	cca Pro	att Ile	cct Pro	att Ile	ttc Phe	ttt Phe	aat Asn	caa Gln	gga Gly	atg Met	gga Gly	gat Asp	tct Ser	act Thr	ttg Leu	4505	
1255			1260						1265						1270		
gag Glu	ttc Phe	cat His	tcc Ser	atc Ile	ctg Leu	agt Ser	ttt Phe	ggc Gly	gtt Val	gag Glu	tct Ser	tcg Ser	att Ile	aaa Lys	tat Tyr	4553	
			1275						1280						1285		
tca Ser	aat Asn	agc Ser	atc Ile	aag Lys	gaa Glu	atg Met	gtt Val	att Ile	ctc Leu	ttt Phe	gcc Ala	aca Thr	aca Thr	att Ile	tat Tyr	4601	
1290			1295						1300								
aga Arg	att Ile	gga Gly	ttg Leu	aaa Lys	gtg Val	cca Pro	cct Pro	gat Asp	gaa Glu	agg Arg	gat Asp	cct Pro	cga Arg	gtc Val	ccc Pro	4649	
1305			1310						1315								

atg	ctg	acc	tgg	agc	acc	tgc	gct	ttc	act	atc	cag	gca	att	gaa	aat	4697
Met	Leu	Thr	Trp	Ser	Thr	Cys	Ala	Phe	Thr	Ile	Gln	Ala	Ile	Glu	Asn	
1320			1325			1330										
cta	ttg	gga	gat	gaa	gga	aaa	cct	ctg	ttt	gga	gca	ctt	caa	aat	agg	4745
Leu	Leu	Gly	Asp	Glu	Gly	Lys	Pro	Leu	Phe	Gly	Ala	Leu	Gln	Asn	Arg	
1335			1340			1345			1350							
cag	cat	aat	ggg	ctg	aaa	gca	tta	atg	cag	ttt	gca	gtt	gca	cag	agg	4793
Gln	His	Asn	Gly	Leu	Lys	Ala	Leu	Met	Gln	Phe	Ala	Val	Ala	Gln	Arg	
1355			1360			1365										
att	acc	tgt	cct	cag	gtc	ctg	ata	cag	aaa	cat	ctg	gtt	cgt	ctt	cta	4841
Ile	Thr	Cys	Pro	Gln	Val	Leu	Ile	Gln	Lys	His	Leu	Val	Arg	Leu	Leu	
1370			1375			1380										
tca	gtt	gtt	ctt	cct	aac	ata	aaa	tca	gaa	gat	aca	cca	tgc	ctt	ctg	4889
Ser	Val	Val	Leu	Pro	Asn	Ile	Lys	Ser	Glu	Asp	Thr	Pro	Cys	Leu	Leu	
1385			1390			1395										
tct	gtt	gat	ctg	ttt	cat	gtt	ttg	gtg	ggg	gct	gtg	tta	gca	ttc	cca	4937
Ser	Ile	Asp	Leu	Phe	His	Val	Leu	Val	Gly	Ala	Val	Leu	Ala	Phe	Pro	
1400			1405			1410										
tcc	ttg	tat	tgg	gat	gac	cct	gtt	gat	ctg	cag	cct	tct	tca	gtt	agt	4985
Ser	Leu	Tyr	Trp	Asp	Asp	Pro	Val	Asp	Leu	Gln	Pro	Ser	Ser	Val	Ser	
1415			1420			1425							1430			
tct	tcc	tat	aac	cac	ctt	tat	ctc	ttc	cat	ttg	atc	acc	atg	gca	cac	5033
Ser	Ser	Tyr	Asn	His	Leu	Tyr	Leu	Phe	His	Leu	Ile	Thr	Met	Ala	His	
1435			1440			1445										
atg	ctt	cag	ata	cta	ctt	aca	gta	gac	aca	ggc	cta	ccc	ctt	gct	cag	5081
Met	Leu	Gln	Ile	Leu	Leu	Thr	Val	Asp	Thr	Gly	Leu	Pro	Leu	Ala	Gln	
1450			1455			1460										
gtt	caa	gaa	gac	agt	gaa	gag	gct	cat	tcc	gca	tct	tct	ttc	ttt	gca	5129
Val	Gln	Glu	Asp	Ser	Glu	Glu	Ala	His	Ser	Ala	Ser	Ser	Phe	Phe	Ala	
1465			1470			1475										
gaa	att	tct	caa	tat	aca	agt	ggc	tcc	att	ggg	tgt	gat	att	cct	ggc	5177
Glu	Ile	Ser	Gln	Tyr	Thr	Ser	Gly	Ser	Ile	Gly	Cys	Asp	Ile	Pro	Gly	
1480			1485			1490										
tgg	tat	ttg	tgg	gtc	tca	ctg	aag	aat	ggc	atc	acc	cct	tat	ctt	cgc	5225
Trp	Tyr	Leu	Trp	Val	Ser	Leu	Lys	Asn	Gly	Ile	Thr	Pro	Tyr	Leu	Arg	
1495			1500			1505							1510			
tgt	gct	gca	ttg	ttt	ttc	cac	tat	tta	ctt	ggg	gta	act	ccg	cct	gag	5273
Cys	Ala	Ala	Leu	Phe	Phe	His	Tyr	Leu	Leu	Gly	Val	Thr	Pro	Pro	Glu	
1515			1520			1525										
gaa	ctg	cat	acc	aat	tct	gca	gaa	gga	gag	tac	agt	gca	ctc	tgt	agc	5321
Glu	Leu	His	Thr	Asn	Ser	Ala	Glu	Gly	Glu	Tyr	Ser	Ala	Leu	Cys	Ser	
1530			1535			1540										
tat	cta	tct	tta	cct	aca	aat	ttg	ttc	ctg	ctc	ttc	cag	gaa	tat	tgg	5369
Tyr	Leu	Ser	Leu	Pro	Thr	Asn	Leu	Phe	Leu	Leu	Phe	Gln	Glu	Tyr	Trp	
1545			1550			1555										

```
<210> 2
<211> 1749
<212> PRT
<213> Homo sapiens
```


Met	Ala	Asp	Glu	Ala	Gly	Gly	Thr	Glu	Arg	Met	Glu	Ile	Ser	Ala	
1			5					10					15		
Glu	Leu	Pro	Gln	Thr	Pro	Gln	Arg	Leu	Ala	Ser	Trp	Trp	Asp	Gln	Gln
			20					25					30		
Val	Asp	Phe	Tyr	Thr	Ala	Phe	Leu	His	His	Leu	Ala	Gln	Leu	Val	Pro
		35					40					45			
Glu	Ile	Tyr	Phe	Ala	Glu	Met	Asp	Pro	Asp	Leu	Glu	Lys	Gln	Glu	Glu
		50				55					60				
Ser	Val	Gln	Met	Ser	Ile	Phe	Thr	Pro	Leu	Glu	Trp	Tyr	Leu	Phe	Gly
65					70					75					80
Glu	Asp	Pro	Asp	Ile	Cys	Leu	Glu	Lys	Leu	Lys	His	Ser	Gly	Ala	Phe
				85					90					95	
Gln	Leu	Cys	Gly	Arg	Val	Phe	Lys	Ser	Gly	Glu	Thr	Thr	Tyr	Ser	Cys
			100					105					110		
Arg	Asp	Cys	Ala	Ile	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Asp	Cys	Phe
		115					120					125			
Gln	Asp	Ser	Val	His	Lys	Asn	His	Arg	Tyr	Lys	Met	His	Thr	Ser	Thr
		130				135					140				
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Thr	Gly
145					150					155					160
Pro	Phe	Cys	Val	Asn	His	Glu	Pro	Gly	Arg	Ala	Gly	Thr	Ile	Lys	Glu
				165					170					175	
Asn	Ser	Arg	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	Val	Gln	Ala	Arg	Lys
			180					185					190		
Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Val	Val	Glu	Met	Thr	Ile	Trp	Glu
		195					200					205			
Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu
		210				215					220				
Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His
225					230					235					240
Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala
				245					250					255	
Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys
			260					265					270		
Ala	Gly	Ala	Tyr	Ala	Ala	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser
		275					280					285			
His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His
		290				295					300				
Ser	Glu	Ile	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp
305					310					315					320
Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys
				325					330					335	

Gln	Ala	Cys	Leu	Arg	Glu	Glu	Pro	Asp	Ser	Glu	Asn	Pro	Cys	Leu	Ile			
			340					345					350					
Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys			
		355					360					365						
Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr			
	370					375					380							
Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln			
385					390					395					400			
Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Asp	Arg	Ser	Ile	Ser	Ile	Thr	Ala			
				405					410					415				
Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile			
			420					425					430					
Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val			
		435					440					445						
Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe	Asn	Phe	Gln	Gly	Tyr			
	450				455						460							
Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val	Ile	Cys	Asp	Leu	Lys			
465					470					475					480			
Tyr	Ile	Leu	Ile	Ser	Lys	Pro	Thr	Ile	Trp	Thr	Glu	Arg	Leu	Arg	Met			
				485					490					495				
Gln	Phe	Leu	Glu	Gly	Phe	Arg	Ser	Phe	Leu	Lys	Ile	Leu	Thr	Cys	Met			
		500						505					510					
Gln	Gly	Met	Glu	Glu	Ile	Arg	Arg	Gln	Val	Gly	Gln	His	Ile	Glu	Val			
		515					520					525						
Asp	Pro	Asp	Trp	Glu	Ala	Ala	Ile	Ala	Ile	Gln	Met	Gln	Leu	Lys	Asn			
	530					535					540							
Ile	Leu	Leu	Met	Phe	Gln	Glu	Trp	Cys	Ala	Cys	Asp	Glu	Glu	Leu	Leu			
545				550						555					560			
Leu	Val	Ala	Tyr	Lys	Glu	Cys	His	Lys	Ala	Val	Met	Arg	Cys	Ser	Thr			
				565					570					575				
Ser	Phe	Ile	Ser	Ser	Ser	Lys	Thr	Val	Val	Gln	Ser	Cys	Gly	His	Ser			
			580					585					590					
Leu	Glu	Thr	Lys	Ser	Tyr	Arg	Val	Ser	Glu	Asp	Leu	Val	Ser	Ile	His			
		595					600					605						
Leu	Pro	Leu	Ser	Arg	Thr	Leu	Ala	Gly	Leu	His	Val	Arg	Leu	Ser	Arg			
	610					615					620							
Leu	Gly	Ala	Val	Ser	Arg	Leu	His	Glu	Phe	Val	Ser	Phe	Glu	Asp	Phe			
625					630					635					640			
Gln	Val	Glu	Val	Leu	Val	Glu	Tyr	Pro	Leu	Arg	Cys	Leu	Val	Leu	Val			
				645					650					655				
Ala	Gln	Val	Val	Ala	Glu	Met	Trp	Arg	Arg	Asn	Gly	Leu	Ser	Leu	Ile			
			660					665					670					

Ser	Gln	Val	Phe	Tyr	Tyr	Gln	Asp	Val	Lys	Cys	Arg	Glu	Glu	Met	Tyr
		675					680					685			
Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala	Ser	Leu	Met	Asp	Pro
	690					695					700				
Asn	Lys	Phe	Leu	Leu	Leu	Val	Leu	Gln	Arg	Tyr	Glu	Leu	Ala	Glu	Ala
705					710					715					720
Phe	Asn	Lys	Thr	Ile	Ser	Thr	Lys	Asp	Gln	Asp	Leu	Ile	Lys	Gln	Tyr
				725					730					735	
Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	Ile	Tyr	Ile	Val	Gly
			740					745					750		
Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr	Lys	Glu	Glu	Val	Thr
		755					760					765			
Met	Arg	Glu	Ile	Ile	His	Leu	Leu	Cys	Ile	Glu	Pro	Met	Pro	His	Ser
	770					775					780				
Ala	Ile	Ala	Lys	Asn	Leu	Pro	Glu	Asn	Glu	Asn	Asn	Glu	Thr	Gly	Leu
785					790					795					800
Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys	Lys	Pro	Gly	Val	Ser
				805					810					815	
Gly	His	Gly	Val	Tyr	Glu	Leu	Lys	Asp	Glu	Ser	Leu	Lys	Asp	Phe	Asn
			820					825					830		
Met	Tyr	Phe	Tyr	His	Tyr	Ser	Lys	Thr	Gln	His	Ser	Lys	Ala	Glu	His
		835					840					845			
Met	Gln	Lys	Lys	Arg	Arg	Lys	Gln	Glu	Asn	Lys	Asp	Glu	Ala	Leu	Pro
	850					855					860				
Pro	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	Ser	Lys	Val	Ile	Asn
865					870					875					880
Leu	Leu	Asn	Cys	Asp	Ile	Met	Met	Tyr	Ile	Leu	Arg	Thr	Val	Phe	Glu
				885					890					895	
Arg	Ala	Ile	Asp	Thr	Asp	Ser	Asn	Leu	Trp	Thr	Glu	Gly	Met	Leu	Gln
			900					905					910		
Met	Ala	Phe	His	Ile	Leu	Ala	Leu	Gly	Leu	Leu	Glu	Glu	Lys	Gln	Gln
		915					920					925			
Leu	Gln	Lys	Ala	Pro	Glu	Glu	Glu	Val	Thr	Phe	Asp	Phe	Tyr	His	Lys
	930					935					940				
Ala	Ser	Arg	Leu	Gly	Ser	Ser	Ala	Met	Asn	Ile	Gln	Met	Leu	Leu	Glu
945					950					955					960
Lys	Leu	Lys	Gly	Ile	Pro	Gln	Leu	Glu	Gly	Gln	Lys	Asp	Met	Ile	Thr
				965					970					975	
Trp	Ile	Leu	Gln	Met	Phe	Asp	Thr	Val	Lys	Arg	Leu	Arg	Glu	Lys	Ser
			980					985					990		
Cys	Leu	Ile	Val	Ala	Thr	Thr	Ser	Gly	Ser	Glu	Ser	Ile	Lys	Asn	Asp
		995					1000					1005			

Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg Lys Arg Lys Ala Glu
 1010 1015 1020
 Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala Gln Met Ser Ala Leu
 025 1030 1035 1040
 Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met Tyr Asp Asn Thr Ser
 1045 1050 1055
 Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu Glu Glu Ser Thr Pro
 1060 1065 1070
 Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly Pro Lys Arg Gly Pro
 1075 1080 1085
 Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys Gln Glu Glu
 1090 1095 1100
 Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val Leu Ser Ala Cys Val
 105 1110 1115 1120
 Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly Lys Pro Ile Glu Leu
 1125 1130 1135
 Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp Pro Asp Leu Ala Tyr
 1140 1145 1150
 Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met His Ala Val Cys Trp
 1155 1160 1165
 Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser Gln Gln Arg Ile His
 1170 1175 1180
 Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr Leu Cys Pro Leu Cys
 185 1190 1195 1200
 Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile Pro Leu Gln Pro Gln
 1205 1210 1215
 Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala Gln Leu Leu Thr Leu
 1220 1225 1230
 Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile Ser Gly Tyr Asn Ile
 1235 1240 1245
 Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile Phe Phe Asn Gln Gly
 1250 1255 1260
 Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile Leu Ser Phe Gly Val
 265 1270 1275 1280
 Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys Glu Met Val Ile Leu
 1285 1290 1295
 Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys Val Pro Pro Asp Glu
 1300 1305 1310
 Arg Asp Pro Arg Val Pro Met Leu Thr Trp Ser Thr Cys Ala Phe Thr
 1315 1320 1325
 Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu Gly Lys Pro Leu Phe
 1330 1335 1340

Gly Ala Leu Gln Asn Arg Gln His Asn Gly Leu Lys Ala Leu Met Gln
345 1350 1355 1360

Phe Ala Val Ala Gln Arg Ile Thr Cys Pro Gln Val Leu Ile Gln Lys
1365 1370 1375

His Leu Val Arg Leu Leu Ser Val Val Leu Pro Asn Ile Lys Ser Glu
1380 1385 1390

Asp Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe His Val Leu Val Gly
1395 1400 1405

Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp Asp Pro Val Asp Leu
1410 1415 1420

Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His Leu Tyr Leu Phe His
425 1430 1435 1440

Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu Thr Val Asp Thr
1445 1450 1455

Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser Glu Glu Ala His Ser
1460 1465 1470

Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr Thr Ser Gly Ser Ile
1475 1480 1485

Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp Val Ser Leu Lys Asn Gly
1490 1495 1500

Ile Thr Pro Tyr Leu Arg Cys Ala Ala Leu Phe Phe His Tyr Leu Leu
505 1510 1515 1520

Gly Val Thr Pro Pro Glu Glu Leu His Thr Asn Ser Ala Glu Gly Glu
1525 1530 1535

Tyr Ser Ala Leu Cys Ser Tyr Leu Ser Leu Pro Thr Asn Leu Phe Leu
1540 1545 1550

Leu Phe Gln Glu Tyr Trp Asp Thr Val Arg Pro Leu Leu Gln Arg Trp
1555 1560 1565

Cys Ala Asp Pro Ala Leu Leu Asn Cys Leu Lys Gln Lys Asn Thr Val
1570 1575 1580

Val Arg Tyr Pro Arg Lys Arg Asn Ser Leu Ile Glu Leu Pro Asp Asp
585 1590 1595 1600

Tyr Ser Cys Leu Leu Asn Gln Ala Ser His Phe Arg Cys Pro Arg Ser
1605 1610 1615

Ala Asp Asp Glu Arg Lys His Pro Val Leu Cys Leu Phe Cys Gly Ala
1620 1625 1630

Ile Leu Cys Ser Gln Asn Ile Cys Cys Gln Glu Ile Val Asn Gly Glu
1635 1640 1645

Glu Val Gly Ala Cys Ile Phe His Ala Leu His Cys Gly Ala Gly Val
1650 1655 1660

Cys Ile Phe Leu Lys Ile Arg Glu Cys Arg Val Val Leu Val Glu Gly
665 1670 1675 1680

665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Lys Ala Arg Gly Cys Ala Tyr Pro Ala Pro Tyr Leu Asp Glu Tyr Gly
1685 1690 1695

Glu Thr Asp Pro Gly Leu Lys Arg Gly Asn Pro Leu His Leu Ser Arg
1700 1705 1710

Glu Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile Ile
1715 1720 1725

Glu Glu Ile Ala Arg Ser Gln Glu Thr Asn Gln Met Leu Phe Gly Phe
1730 1735 1740

Asn Trp Gln Leu Leu
745

<210> 3
<211> 6300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (295)..(5559)

<400> 3
gccaagaatt cggcaccgagg tgtcaggcct ggggttttct gtgtccttcc ctgggtcagg 60
gacgagccag tgacttgact cttgggcgct aagcttggga gggagcgcag gaggccgctg 120
tccttccttt ccggttcacg tcacccttct ctccctctgt tgctccacct gcagccactt 180
ggacggctcc gggactgatt gcctggggca ggggtggcag tcgaggccgc cggggccgag 240
gtgaggctgc agctctccgg gcggcggtag cgctggggag gaggaggaga gaag atg 297
Met
1
gcg tcg gag cta gag cca gag gtg cag gcc atc gac cgg agt ttg ctg 345
Ala Ser Glu Leu Glu Pro Glu Val Gln Ala Ile Asp Arg Ser Leu Leu
5 10 15
gaa tgt tcg gcc gag gag att gcg ggg aaa tgg ctg caa gca act gac 393
Glu Cys Ser Ala Glu Glu Ile Ala Gly Lys Trp Leu Gln Ala Thr Asp
20 25 30
ctc act aga gaa gtg tac cag cat tta gcc cac tat gta ccc aaa atc 441
Leu Thr Arg Glu Val Tyr Gln His Leu Ala His Tyr Val Pro Lys Ile
35 40 45
tac tgc agg ggt ccc aac cct ttt cca cag aaa gaa gac atg ctg gca 489
Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu Ala
50 55 60 65
cag cat gtt ttg ttg gga cca atg gaa tgg tac ctt tgt ggt gaa gat 537
Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu Asp
70 75 80
cct gca ttt gga ttt cca aaa ctt gag caa gca aac aaa cct tct cat 585
Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser His
85 90 95

ctt	tgt	ggt	cgt	gtt	ttt	aaa	gta	gga	gag	cct	aca	tat	tct	tgc	aga	633
Leu	Cys	Gly	Arg	Val	Phe	Lys	Val	Gly	Glu	Pro	Thr	Tyr	Ser	Cys	Arg	
		100					105					110				
gac	tgt	gca	gtt	gat	cca	act	tgt	gtt	ttg	tgc	atg	gag	tgc	ttt	ttg	681
Asp	Cys	Ala	Val	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Glu	Cys	Phe	Leu	
	115					120					125					
gga	agt	att	cac	aga	gat	cat	cga	tat	agg	atg	aca	aca	tca	gga	ggt	729
Gly	Ser	Ile	His	Arg	Asp	His	Arg	Tyr	Arg	Met	Thr	Thr	Ser	Gly	Gly	
130					135				140					145		
gga	ggt	ttc	tgt	gac	tgt	ggt	gat	act	gaa	gcc	tgg	aaa	gag	ggt	cct	777
Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Glu	Gly	Pro	
			150						155					160		
tac	tgt	caa	aaa	cat	gaa	ctt	aac	acc	tct	gaa	att	gag	gaa	gaa	gag	825
Tyr	Cys	Gln	Lys	His	Glu	Leu	Asn	Thr	Ser	Glu	Ile	Glu	Glu	Glu	Glu	
		165					170					175				
gat	cct	ctt	gtt	cat	tta	tca	gaa	gat	gtg	ata	gca	aga	act	tat	aac	873
Asp	Pro	Leu	Val	His	Leu	Ser	Glu	Asp	Val	Ile	Ala	Arg	Thr	Tyr	Asn	
		180					185					190				
att	ttt	gct	att	acg	ttt	cgg	tat	gca	gta	gaa	ata	tta	acc	tgg	gaa	921
Ile	Phe	Ala	Ile	Thr	Phe	Arg	Tyr	Ala	Val	Glu	Ile	Leu	Thr	Trp	Glu	
	195					200					205					
aaa	gaa	agt	gaa	ttg	cca	gca	gat	tta	gag	atg	gta	gag	aag	agt	gac	969
Lys	Glu	Ser	Glu	Leu	Pro	Ala	Asp	Leu	Glu	Met	Val	Glu	Lys	Ser	Asp	
210					215					220				225		
acc	tac	tat	tgc	atg	ctg	ttt	aat	gat	gag	gtt	cac	acc	tat	gaa	caa	1017
Thr	Tyr	Tyr	Cys	Met	Leu	Phe	Asn	Asp	Glu	Val	His	Thr	Tyr	Glu	Gln	
			230						235					240		
gtt	att	tat	act	ctt	cag	aaa	gct	gtt	aac	tgt	aca	caa	aaa	gaa	gct	1065
Val	Ile	Tyr	Thr	Leu	Gln	Lys	Ala	Val	Asn	Cys	Thr	Gln	Lys	Glu	Ala	
			245					250					255			
att	ggt	ttt	gca	act	aca	gta	gat	cga	gat	ggg	cgt	agg	tct	gtt	cga	1113
Ile	Gly	Phe	Ala	Thr	Thr	Val	Asp	Arg	Asp	Gly	Arg	Arg	Ser	Val	Arg	
		260					265					270				
tat	gga	gat	ttt	cag	tat	tgt	gag	caa	gca	aaa	tca	gta	att	gtg	aga	1161
Tyr	Gly	Asp	Phe	Gln	Tyr	Cys	Glu	Gln	Ala	Lys	Ser	Val	Ile	Val	Arg	
	275					280					285					
aat	acc	agt	aga	cag	aca	aag	cca	ctc	aaa	gtt	caa	gtt	atg	cat	tcg	1209
Asn	Thr	Ser	Arg	Gln	Thr	Lys	Pro	Leu	Lys	Val	Gln	Val	Met	His	Ser	
290					295					300				305		
tct	att	gtc	gca	cat	cag	aat	ttt	ggt	ttg	aaa	ctt	ttg	tct	tgg	ctg	1257
Ser	Ile	Val	Ala	His	Gln	Asn	Phe	Gly	Leu	Lys	Leu	Leu	Ser	Trp	Leu	
				310					315					320		
gga	agt	att	att	gga	tat	tca	gat	ggc	ctt	cgc	cgg	att	tta	tgt	caa	1305
Gly	Ser	Ile	Ile	Gly	Tyr	Ser	Asp	Gly	Leu	Arg	Arg	Ile	Leu	Cys	Gln	
			325					330					335			
gtt	ggt	tta	caa	gaa	ggg	cca	gat	ggt	gaa	aac	tct	tct	cta	gtg	gac	1353
Val	Gly	Leu	Gln	Glu	Gly	Pro	Asp	Gly	Glu	Asn	Ser	Ser	Leu	Val	Asp	
		340					345					350				

aga Arg	ctg Leu	atg Met	ctt Leu	agt Ser	gat Asp	tcc Ser	aaa Lys	tta Leu	tgg Trp	aaa Lys	ggt Gly	gct Ala	agg Arg	agt Ser	gta Val	1401
tat Tyr	cat His	cag Gln	ttg Leu	ttc Phe	atg Met	agc Ser	agt Ser	ctg Leu	ctt Leu	atg Met	gat Asp	ttg Leu	aaa Lys	tac Tyr	aag Lys	1449
aaa Lys	cta Leu	ttt Phe	gct Ala	gtt Val	cga Arg	ttt Phe	gca Ala	aaa Lys	aat Asn	tac Tyr	cag Gln	cag Gln	ttg Leu	cag Gln	aga Arg	1497
gat Asp	ttt Phe	atg Met	gag Glu	gat Asp	gat Asp	cac His	gag Glu	cga Arg	gca Ala	gtg Val	tcg Ser	gtg Val	act Thr	gct Ala	cta Leu	1545
tct Ser	gtc Val	cag Gln	ttc Phe	ttc Phe	acc Thr	gca Ala	cct Pro	act Thr	ctg Leu	gct Ala	cga Arg	atg Met	ctc Leu	atc Ile	aca Thr	1593
gaa Glu	gaa Glu	aac Asn	ttg Leu	atg Met	agc Ser	att Ile	atc Ile	att Ile	aag Lys	act Thr	ttt Phe	atg Met	gat Asp	cat His	ttg Leu	1641
aga Arg	cat His	cga Arg	gat Asp	gcc Ala	cag Gln	ggc Gly	aga Arg	ttt Phe	cag Gln	ttt Phe	gaa Glu	cga Arg	tac Tyr	act Thr	gct Ala	1689
tta Leu	caa Gln	gcc Ala	ttc Phe	aaa Lys	ttt Phe	agg Arg	aga Arg	gta Val	cag Gln	agc Ser	ctt Leu	att Ile	tta Leu	gat Asp	ctc Leu	1737
aag Lys	tat Tyr	gtg Val	tta Leu	att Ile	agc Ser	aaa Lys	cca Pro	act Thr	gaa Glu	tgg Trp	tca Ser	gat Asp	gag Glu	ctg Leu	agg Arg	1785
cag Gln	aag Lys	ttc Phe	cta Leu	gaa Glu	ggg Gly	ttt Phe	gat Asp	gcc Ala	ttt Phe	ttg Leu	gaa Glu	tta Leu	cta Leu	aaa Lys	tgt Cys	1833
atg Met	cag Gln	gga Gly	atg Met	gat Asp	cca Pro	att Ile	aca Thr	cgt Arg	caa Gln	gta Val	gga Gly	caa Gln	cat His	att Ile	gaa Glu	1881
atg Met	gaa Glu	cca Pro	gag Glu	tgg Trp	gaa Glu	gca Ala	gcc Ala	ttc Phe	aca Thr	cta Leu	caa Gln	atg Met	aaa Lys	tta Leu	aca Thr	1929
cat His	gtc Val	att Ile	tca Ser	atg Met	atg Met	cag Gln	gac Asp	tgg Trp	tgt Cys	gct Ala	tca Ser	gat Asp	gaa Glu	aaa Lys	gtg Val	1977
tta Leu	atc Ile	gaa Glu	gct Ala	tac Tyr	aag Lys	aaa Lys	tgt Cys	ctc Leu	gct Ala	gta Val	ctg Leu	atg Met	cag Gln	tgt Cys	cat His	2025
ggt Gly	ggt Gly	tat Tyr	act Thr	gat Asp	ggt Gly	gaa Glu	cag Gln	cca Pro	atc Ile	aca Thr	cta Leu	agc Ser	att Ile	tgt Cys	gga Gly	2073
cat His	tca Ser	gtg Val	gaa Glu	act Thr	atc Ile	aga Arg	tac Tyr	tgt Cys	gtt Val	tcc Ser	caa Gln	gaa Glu	aaa Lys	gtt Val	agc Ser	2121

att Ile 610	cac His	ctc Leu	cca Pro	gtt Val	tct Ser 615	cgc Arg	tta Leu	ctt Leu	gca Ala	ggt Gly 620	tta Leu	cat His	gta Val	tta Leu 625	tta Leu	2169
agc Ser	aaa Lys	agt Ser	gaa Glu	gtg Val 630	gca Ala	tat Tyr	aaa Lys	ttt Phe	cca Pro 635	gag Glu	ctc Leu	cta Leu	cct Pro	cta Leu 640	agt Ser	2217
gaa Glu	ctt Leu	agc Ser	cca Pro 645	ccc Pro	atg Met	ttg Leu	ata Ile	gaa Glu 650	cac His	cct Pro	ctt Leu	aga Arg	tgt Cys 655	ctt Leu	gtt Val	2265
ctg Leu	tgt Cys	gcc Ala 660	caa Gln	gta Val	cat His	gcc Ala	gga Gly 665	atg Met	tgg Trp	aga Arg	aga Arg	aat Asn 670	ggg Gly	ttc Phe	tct Ser	2313
cta Leu	gta Val 675	aac Asn	cag Gln	att Ile	tat Tyr	tac Tyr 680	tac Tyr	cat His	aat Asn	gtg Val	aaa Lys 685	tgc Cys	aga Arg	cgt Arg	gag Glu	2361
atg Met 690	ttt Phe	gac Asp	aag Lys	gat Asp	gta Val 695	gta Val	atg Met	ctt Leu	cag Gln	aca Thr 700	ggt Gly	gtc Val	tcc Ser	atg Met	atg Met 705	2409
gat Asp	cca Pro	aat Asn	cat His 710	ttc Phe	ctg Leu	atg Met	atc Ile	atg Met	ctc Leu 715	agc Ser	cgc Arg	ttt Phe	gaa Glu	ctt Leu 720	tat Tyr	2457
cag Gln	att Ile	ttc Phe 725	agt Ser	act Thr	cca Pro	gac Asp	tat Tyr	gga Gly 730	aaa Lys	aga Arg	ttt Phe	agt Ser	tct Ser 735	gag Glu	att Ile	2505
acc Thr	cat His	aag Lys 740	gat Asp	gtt Val	gtt Val	cag Gln	cag Gln 745	aac Asn	aat Asn	act Thr	cta Leu	ata Ile 750	gaa Glu	gaa Glu	atg Met	2553
cta Leu 755	tac Tyr	ctc Leu	att Ile	ata Ile	atg Met	ctt Leu 760	gtt Val	gga Gly	gag Glu	aga Arg	ttt Phe 765	agt Ser	cct Pro	gga Gly	gtt Val	2601
gga Gly 770	cag Gln	gta Val	aat Asn	gct Ala	aca Thr 775	gat Asp	gaa Glu	atc Ile	aag Lys	cga Arg 780	gag Glu	att Ile	atc Ile	cat His	cag Gln 785	2649
ttg Leu	agt Ser	atc Ile	aag Lys	cct Pro 790	atg Met	gct Ala	cat His	agt Ser	gaa Glu 795	ttg Leu	gta Val	aag Lys	tct Ser	tta Leu 800	cct Pro	2697
gaa Glu	gat Asp	gag Glu	aac Asn 805	aag Lys	gag Glu	act Thr	ggc Gly 810	atg Met	gag Glu	agt Ser	gta Val	atc Ile	gaa Glu 815	gca Ala	gtt Val	2745
gcc Ala	cat His 820	ttc Phe	aag Lys	aaa Lys	cct Pro	gga Gly	tta Leu 825	aca Thr	gga Gly	cga Arg	ggc Gly	atg Met 830	tat Tyr	gaa Glu	ctg Leu	2793
aaa Lys	cca Pro 835	gaa Glu	tgt Cys	gcc Ala	aaa Lys	gag Glu 840	ttc Phe	aac Asn	ttg Leu	tat Tyr	ttc Phe 845	tat Tyr	cac His	ttt Phe	tca Ser	2841
agg Arg 850	gca Ala	gaa Glu	cag Gln	tcc Ser	aag Lys 855	gca Ala	gaa Glu	gaa Glu	gcg Ala 860	caa Gln	cgg Arg	aaa Lys	ttg Leu	aaa Lys	aga Arg 865	2889

caa aat aga gaa gat aca gca ctc cca cct ccg gtg ttg cct cca ttc	2937
Gln Asn Arg Glu Asp Thr Ala Leu Pro Pro Pro Val Leu Pro Pro Phe	
870 875 880	
tgc cct ctg ttt gca agc ctg gtt aac att ttg cag tca gat gtc atg	2985
Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Ser Asp Val Met	
885 890 895	
ttg tgc atc atg gga aca att ctg caa tgg gct gtg gaa cat aat gga	3033
Leu Cys Ile Met Gly Thr Ile Leu Gln Trp Ala Val Glu His Asn Gly	
900 905 910	
tat gcc tgg tca gag tcc atg ctg caa agg gtg tta cat tta att ggc	3081
Tyr Ala Trp Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile Gly	
915 920 925	
atg gca cta caa gaa gaa aaa caa cat tta gag aat gtc acg gaa gag	3129
Met Ala Leu Gln Glu Glu Lys Gln His Leu Glu Asn Val Thr Glu Glu	
930 935 940 945	
cat gta gta aca ttt acc ttc act cag aag ata tca aaa cct ggt gaa	3177
His Val Val Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly Glu	
950 955 960	
gcg cca aaa aat tct cct agc ata cta gct atg ctg gaa aca cta caa	3225
Ala Pro Lys Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu Gln	
965 970 975	
aat gct ccc tac cta gaa gtc cac aaa gac atg att cgg tgg ata ttg	3273
Asn Ala Pro Tyr Leu Glu Val His Lys Asp Met Ile Arg Trp Ile Leu	
980 985 990	
aag act ttt aat gct gtt aaa aag atg agg gag agt tca cct acc agt	3321
Lys Thr Phe Asn Ala Val Lys Lys Met Arg Glu Ser Ser Pro Thr Ser	
995 1000 1005	
ccc gtg gca gag aca gaa gga acc ata atg gaa gag agt tca agg gac	3369
Pro Val Ala Glu Thr Glu Gly Thr Ile Met Glu Glu Ser Ser Arg Asp	
1010 1015 1020 1025	
aaa gac aaa gct gag agg aag aga aaa gca gag att gcc aga ctg cgc	3417
Lys Asp Lys Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu Arg	
1030 1035 1040	
aga gaa aag atc atg gct cag atg tct gaa atg cag cgg cat ttt att	3465
Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe Ile	
1045 1050 1055	
gat gaa aac aaa gaa ctc ttt cag cag aca tta gaa ctg gat gcc tca	3513
Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Ala Ser	
1060 1065 1070	
acc tct gct gtt ctt gat cat agc cct gtg gct tca gat atg aca ctt	3561
Thr Ser Ala Val Leu Asp His Ser Pro Val Ala Ser Asp Met Thr Leu	
1075 1080 1085	
aca gca ctg ggt ccc aca caa act cag gtt cct gaa caa aga caa ttc	3609
Thr Ala Leu Gly Pro Thr Gln Thr Gln Val Pro Glu Gln Arg Gln Phe	
1090 1095 1100 1105	
gtt aca tgt ata ttg tgt caa gag gag caa gaa gtt aaa gtg gaa agc	3657
Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Lys Val Glu Ser	
1110 1115 1120	

1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120

agg	gca	atg	gtc	ttg	gca	gca	ttt	gtt	cag	aga	tca	act	gta	tta	tca	3705
Arg	Ala	Met	Val	Leu	Ala	Ala	Phe	Val	Gln	Arg	Ser	Thr	Val	Leu	Ser	
			1125					1130					1135			
aaa	aac	aga	agt	aaa	ttt	att	caa	gat	cca	gaa	aaa	tat	gat	cca	tta	3753
Lys	Asn	Arg	Ser	Lys	Phe	Ile	Gln	Asp	Pro	Glu	Lys	Tyr	Asp	Pro	Leu	
			1140				1145					1150				
ttc	atg	cac	cct	gat	ctg	tct	tgt	gga	aca	cac	act	agt	agc	tgt	ggg	3801
Phe	Met	His	Pro	Asp	Leu	Ser	Cys	Gly	Thr	His	Thr	Ser	Ser	Cys	Gly	
			1155				1160					1165				
cac	att	atg	cat	gcc	cat	tgt	tgg	caa	agg	tat	ttt	gat	tcc	gtt	caa	3849
His	Ile	Met	His	Ala	His	Cys	Trp	Gln	Arg	Tyr	Phe	Asp	Ser	Val	Gln	
										1180					1185	
gct	aaa	gaa	cag	cga	agg	caa	cag	aga	tta	cgc	tta	cat	acg	agc	tat	3897
Ala	Lys	Glu	Gln	Arg	Arg	Gln	Gln	Arg	Leu	Arg	Leu	His	Thr	Ser	Tyr	
				1190					1195					1200		
gat	gta	gaa	aac	gga	gaa	ttc	ctt	tgc	ccc	ctt	tgt	gaa	tgc	ttg	agt	3945
Asp	Val	Glu	Asn	Gly	Glu	Phe	Leu	Cys	Pro	Leu	Cys	Glu	Cys	Leu	Ser	
			1205					1210					1215			
aat	act	gtt	att	cct	ctg	ctg	ctt	cct	cca	aga	aat	att	ttt	aac	aac	3993
Asn	Thr	Val	Ile	Pro	Leu	Leu	Leu	Pro	Pro	Arg	Asn	Ile	Phe	Asn	Asn	
			1220				1225						1230			
agg	tta	aat	ttt	tca	gac	caa	cca	aat	ctg	act	cag	tgg	att	aga	aca	4041
Arg	Leu	Asn	Phe	Ser	Asp	Gln	Pro	Asn	Leu	Thr	Gln	Trp	Ile	Arg	Thr	
			1235			1240						1245				
ata	tct	cag	caa	ata	aaa	gca	tta	cag	ttt	ctt	agg	aaa	gaa	gaa	agt	4089
Ile	Ser	Gln	Gln	Ile	Lys	Ala	Leu	Gln	Phe	Leu	Arg	Lys	Glu	Glu	Ser	
					1255					1260					1265	
act	cct	aat	aat	gcc	tct	aca	aag	aat	tca	gaa	aat	gtg	gat	gaa	tta	4137
Thr	Pro	Asn	Asn	Ala	Ser	Thr	Lys	Asn	Ser	Glu	Asn	Val	Asp	Glu	Leu	
				1270					1275					1280		
cag	ctc	cct	gaa	ggg	ttc	agg	cct	gat	ttt	cgt	cct	aag	atc	cct	tat	4185
Gln	Leu	Pro	Glu	Gly	Phe	Arg	Pro	Asp	Phe	Arg	Pro	Lys	Ile	Pro	Tyr	
			1285					1290					1295			
tct	gag	agc	ata	aaa	gaa	atg	cta	acg	aca	ttt	gga	act	gct	acc	tac	4233
Ser	Glu	Ser	Ile	Lys	Glu	Met	Leu	Thr	Thr	Phe	Gly	Thr	Ala	Thr	Tyr	
			1300				1305					1310				
aag	gtg	gga	cta	aag	gtt	cat	ccc	aat	gaa	gag	gat	cct	cgt	gtt	ccc	4281
Lys	Val	Gly	Leu	Lys	Val	His	Pro	Asn	Glu	Glu	Asp	Pro	Arg	Val	Pro	
			1315			1320					1325					
ata	atg	tgt	tgg	ggt	agc	tgc	gcg	tac	acc	atc	caa					

aca Thr	gtg Val	gca Ala	tca Ser	gtt Val	tca Ser	gtg Val	gtg Val	caa Gln	gga Gly	cat His	ttt Phe	tgt Cys	aaa Lys	ctt Leu	ttt Phe	4473
1380				1385				1390								
gca Ala	tca Ser	ctg Leu	gtg Val	cct Pro	aat Asn	gac Asp	agc Ser	cat His	gag Glu	gaa Glu	ctt Leu	cca Pro	tgc Cys	ata Ile	tta Leu	4521
1395				1400				1405								
gat Asp	att Ile	gac Asp	atg Met	ttt Phe	cat His	tta Leu	ttg Leu	gtg Val	ggc Gly	ttg Leu	gtg Val	ctt Leu	gca Ala	ttt Phe	cct Pro	4569
1410				1415				1420				1425				
gcg Ala	ttg Leu	cag Gln	tgt Cys	cag Gln	gat Asp	ttt Phe	tca Ser	ggg Gly	atc Ile	agc Ser	ctt Leu	ggc Gly	act Thr	gga Gly	gac Asp	4617
				1430				1435				1440				
ctt Leu	cac His	att Ile	ttc Phe	cat His	ctg Leu	gtt Val	act Thr	atg Met	gca Ala	cac His	atc Ile	ata Ile	cag Gln	atc Ile	tta Leu	4665
				1445				1450				1455				
ctt Leu	acc Thr	tca Ser	tgt Cys	aca Thr	gaa Glu	gag Glu	aat Asn	ggc Gly	atg Met	gat Asp	caa Gln	gaa Glu	aat Asn	ccc Pro	cct Pro	4713
1460				1465				1470								
tgt Cys	gaa Glu	gaa Glu	gaa Glu	tca Ser	gca Ala	gtt Val	ctt Leu	gct Ala	ttg Leu	tat Tyr	aaa Lys	aca Thr	ctt Leu	cac His	cag Gln	4761
1475				1480				1485								
tat Tyr	acg Thr	gga Gly	agt Ser	gcc Ala	ttg Leu	aaa Lys	gaa Glu	ata Ile	cca Pro	tcc Ser	ggc Gly	tgg Trp	cat His	ctg Leu	tgg Trp	4809
1490				1495				1500				1505				
agg Arg	agt Ser	gtc Val	aga Arg	gct Ala	gga Gly	atc Ile	atg Met	cct Pro	ttc Phe	ctg Leu	aag Lys	tgt Cys	tct Ser	gct Ala	tta Leu	4857
				1510				1515				1520				
ttt Phe	ttt Phe	cat His	tac Tyr	tta Leu	aat Asn	gga Gly	gtt Val	cct Pro	tcc Ser	cca Pro	ccc Pro	gac Asp	att Ile	caa Gln	gtt Val	4905
1525				1530				1535								
cct Pro	gga Gly	aca Thr	agc Ser	cat His	ttt Phe	gaa Glu	cat His	tta Leu	tgt Cys	agc Ser	tat Tyr	ctt Leu	tcc Ser	cta Leu	cca Pro	4953
1540				1545				1550								
aac Asn	aac Asn	ctc Leu	att Ile	tgc Cys	ctt Leu	ttt Phe	caa Gln	gaa Glu	aat Asn	agt Ser	gag Glu	ata Ile	atg Met	aat Asn	tca Ser	5001
1555				1560				1565								
ctg Leu	att Ile	gaa Glu	agt Ser	tgg Trp	tgc Cys	cgt Arg	aac Asn	agt Ser	gaa Glu	gtt Val	aaa Lys	aga Arg	tat Tyr	cta Leu	gaa Glu	5049
1570				1575				1580				1585				
ggc Gly	gaa Glu	aga Arg	gat Asp	gct Ala	ata Ile	aga Arg	tat Tyr	cca Pro	aga Arg	gaa Glu	tct Ser	aac Asn	aaa Lys	tta Leu	ata Ile	5097
				1590				1595				1600				
aac Asn	ctt Leu	cca Pro	gag Glu	gat Asp	tac Tyr	agc Ser	agc Ser	ctc Leu	att Ile	aat Asn	caa Gln	gca Ala	tcc Ser	aat Asn	ttc Phe	5145
1605				1610				1615								
tcg Ser	tgc Cys	ccg Pro	aaa Lys	tca Ser	ggc Gly	ggc Gly	gat Asp	aag Lys	agc Ser	aga Arg	gcc Ala	cca Pro	act Thr	ctg Leu	tgc Cys	5193
1620				1625				1630								

ctt gtg tgc gga tct ctg ctg tgc tcc cag agt tac tgc tgc cag act 5241
 Leu Val Cys Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln Thr
 1635 1640 1645
 gaa ctg gaa ggg gag gat gta gga gcc tgc aca gct cac acc tac tcc 5289
 Glu Leu Glu Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr Ser
 1650 1655 1660 1665
 tgt ggc tct gga gtg ggc atc ttc ctg aga gta cgg gaa tgt cag gtg 5337
 Cys Gly Ser Gly Val Gly Ile Phe Leu Arg Val Arg Glu Cys Gln Val
 1670 1675 1680
 cta ttt tta gct ggc aaa acc aaa ggc tgt ttt tat tct cct cct tac 5385
 Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro Tyr
 1685 1690 1695
 ctt gat gac tat ggg gag acc gac cag gga ctc aga cgg gga aat cct 5433
 Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn Pro
 1700 1705 1710
 tta cat tta tgc aaa gag cga ttc aag aag att cag aag ctc tgg cac 5481
 Leu His Leu Cys Lys Glu Arg Phe Lys Lys Ile Gln Lys Leu Trp His
 1715 1720 1725
 caa cac agt gtc aca gag gaa att gga cat gca cag gaa gcc aat cag 5529
 Gln His Ser Val Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn Gln
 1730 1735 1740 1745
 aca ctg gtt ggc att gac tgg caa cat tta taattattgc accaccaaaa 5579
 Thr Leu Val Gly Ile Asp Trp Gln His Leu
 1750 1755
 aacacaaact tggatttttt taaccagtt ggctttttaa gaaagaaaga agttctgctg 5639
 aatttggaat taaattcttt atttaaactt tccttcccag ttttatagtt tctgggtctg 5699
 aggactgatg aaaatcatct tccatcagca gattttcttg cactggttgc tgtgcccctc 5759
 aaatataatg tcttggtttt taagatcgag caaggagctt ctcttcttag attggatccc 5819
 agcccccttg tgggggtctg actgcatagt cccagccatt atgtgatatt tcacgttatt 5879
 gatgatagtg aaccgtgggt ccgaagctga ctcaacggag gcagggaaca aagtctctgt 5939
 ggtctgttgg gtcatacttc ctggttccac tgagtggccc aacactggga ctgggttggg 5999
 gtccccctctg ctgacaggac cctactccta ggagcaaagt ggttgatttt gaaggcagtg 6059
 ttcccttctc tccattgact atgagagagt tgggggacac acatgcagaa gaagcccgtg 6119
 gggagaaggt ggattcctgg tgtgctggct ggtttttcag ggctgttaga ggtttttttt 6179
 ttcttttttt tttttatggc aagacttttg gctttgagaa aactcactta gagggctttc 6239
 caaaaactta ggatggtcta aaaaattagg atattctttt agaattagga agaaaaatta 6299
 g 6300

<210> 4
 <211> 1755
 <212> PRT
 <213> Homo sapiens

Met	Ala	Ser	Glu	Leu	Glu	Pro	Glu	Val	Gln	Ala	Ile	Asp	Arg	Ser	Leu
1				5					10					15	
Leu	Glu	Cys	Ser	Ala	Glu	Glu	Ile	Ala	Gly	Lys	Trp	Leu	Gln	Ala	Thr
			20					25					30		
Asp	Leu	Thr	Arg	Glu	Val	Tyr	Gln	His	Leu	Ala	His	Tyr	Val	Pro	Lys
		35					40					45			
Ile	Tyr	Cys	Arg	Gly	Pro	Asn	Pro	Phe	Pro	Gln	Lys	Glu	Asp	Met	Leu
	50					55					60				
Ala	Gln	His	Val	Leu	Leu	Gly	Pro	Met	Glu	Trp	Tyr	Leu	Cys	Gly	Glu
65					70					75					80
Asp	Pro	Ala	Phe	Gly	Phe	Pro	Lys	Leu	Glu	Gln	Ala	Asn	Lys	Pro	Ser
				85					90					95	
His	Leu	Cys	Gly	Arg	Val	Phe	Lys	Val	Gly	Glu	Pro	Thr	Tyr	Ser	Cys
			100					105					110		
Arg	Asp	Cys	Ala	Val	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Glu	Cys	Phe
		115					120					125			
Leu	Gly	Ser	Ile	His	Arg	Asp	His	Arg	Tyr	Arg	Met	Thr	Thr	Ser	Gly
	130					135					140				
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Glu	Gly
145					150					155					160
Pro	Tyr	Cys	Gln	Lys	His	Glu	Leu	Asn	Thr	Ser	Glu	Ile	Glu	Glu	Glu
				165					170					175	
Glu	Asp	Pro	Leu	Val	His	Leu	Ser	Glu	Asp	Val	Ile	Ala	Arg	Thr	Tyr
			180					185					190		
Asn	Ile	Phe	Ala	Ile	Thr	Phe	Arg	Tyr	Ala	Val	Glu	Ile	Leu	Thr	Trp
		195					200					205			
Glu	Lys	Glu	Ser	Glu	Leu	Pro	Ala	Asp	Leu	Glu	Met	Val	Glu	Lys	Ser
	210					215					220				
Asp	Thr	Tyr	Tyr	Cys	Met	Leu	Phe	Asn	Asp	Glu	Val	His	Thr	Tyr	Glu
225					230					235					240
Gln	Val	Ile	Tyr	Thr	Leu	Gln	Lys	Ala	Val	Asn	Cys	Thr	Gln	Lys	Glu
				245					250					255	
Ala	Ile	Gly	Phe	Ala	Thr	Thr	Val	Asp	Arg	Asp	Gly	Arg	Arg	Ser	Val
			260					265					270		
Arg	Tyr	Gly	Asp	Phe	Gln	Tyr	Cys	Glu	Gln	Ala	Lys	Ser	Val	Ile	Val
		275					280					285			
Arg	Asn	Thr	Ser	Arg	Gln	Thr	Lys	Pro	Leu	Lys	Val	Gln	Val	Met	His
	290					295					300				
Ser	Ser	Ile	Val	Ala	His	Gln	Asn	Phe	Gly	Leu	Lys	Leu	Leu	Ser	Trp
305					310					315					320
Leu	Gly	Ser	Ile	Ile	Gly	Tyr	Ser	Asp	Gly	Leu	Arg	Arg	Ile	Leu	Cys
				325					330					335	

Gln	Val	Gly	Leu	Gln	Glu	Gly	Pro	Asp	Gly	Glu	Asn	Ser	Ser	Leu	Val
			340					345					350		
Asp	Arg	Leu	Met	Leu	Ser	Asp	Ser	Lys	Leu	Trp	Lys	Gly	Ala	Arg	Ser
		355					360					365			
Val	Tyr	His	Gln	Leu	Phe	Met	Ser	Ser	Leu	Leu	Met	Asp	Leu	Lys	Tyr
	370					375					380				
Lys	Lys	Leu	Phe	Ala	Val	Arg	Phe	Ala	Lys	Asn	Tyr	Gln	Gln	Leu	Gln
385					390					395					400
Arg	Asp	Phe	Met	Glu	Asp	Asp	His	Glu	Arg	Ala	Val	Ser	Val	Thr	Ala
				405					410					415	
Leu	Ser	Val	Gln	Phe	Phe	Thr	Ala	Pro	Thr	Leu	Ala	Arg	Met	Leu	Ile
			420					425					430		
Thr	Glu	Glu	Asn	Leu	Met	Ser	Ile	Ile	Ile	Lys	Thr	Phe	Met	Asp	His
		435					440					445			
Leu	Arg	His	Arg	Asp	Ala	Gln	Gly	Arg	Phe	Gln	Phe	Glu	Arg	Tyr	Thr
	450					455					460				
Ala	Leu	Gln	Ala	Phe	Lys	Phe	Arg	Arg	Val	Gln	Ser	Leu	Ile	Leu	Asp
465					470					475					480
Leu	Lys	Tyr	Val	Leu	Ile	Ser	Lys	Pro	Thr	Glu	Trp	Ser	Asp	Glu	Leu
				485					490					495	
Arg	Gln	Lys	Phe	Leu	Glu	Gly	Phe	Asp	Ala	Phe	Leu	Glu	Leu	Leu	Lys
			500					505					510		
Cys	Met	Gln	Gly	Met	Asp	Pro	Ile	Thr	Arg	Gln	Val	Gly	Gln	His	Ile
		515					520					525			
Glu	Met	Glu	Pro	Glu	Trp	Glu	Ala	Ala	Phe	Thr	Leu	Gln	Met	Lys	Leu
		530				535					540				
Thr	His	Val	Ile	Ser	Met	Met	Gln	Asp	Trp	Cys	Ala	Ser	Asp	Glu	Lys
545					550					555					560
Val	Leu	Ile	Glu	Ala	Tyr	Lys	Lys	Cys	Leu	Ala	Val	Leu	Met	Gln	Cys
				565					570					575	
His	Gly	Gly	Tyr	Thr	Asp	Gly	Glu	Gln	Pro	Ile	Thr	Leu	Ser	Ile	Cys
			580					585					590		
Gly	His	Ser	Val	Glu	Thr	Ile	Arg	Tyr	Cys	Val	Ser	Gln	Glu	Lys	Val
		595					600					605			
Ser	Ile	His	Leu	Pro	Val	Ser	Arg	Leu	Leu	Ala	Gly	Leu	His	Val	Leu
	610					615					620				
Leu	Ser	Lys	Ser	Glu	Val	Ala	Tyr	Lys	Phe	Pro	Glu	Leu	Leu	Pro	Leu
625					630					635					640
Ser	Glu	Leu	Ser	Pro	Pro	Met	Leu	Ile	Glu	His	Pro	Leu	Arg	Cys	Leu
				645					650					655	
Val	Leu	Cys	Ala	Gln	Val	His	Ala	Gly	Met	Trp	Arg	Arg	Asn	Gly	Phe
			660					665					670		

Ser	Leu	Val	Asn	Gln	Ile	Tyr	Tyr	Tyr	His	Asn	Val	Lys	Cys	Arg	Arg
		675					680					685			
Glu	Met	Phe	Asp	Lys	Asp	Val	Val	Met	Leu	Gln	Thr	Gly	Val	Ser	Met
	690					695					700				
Met	Asp	Pro	Asn	His	Phe	Leu	Met	Ile	Met	Leu	Ser	Arg	Phe	Glu	Leu
705					710					715					720
Tyr	Gln	Ile	Phe	Ser	Thr	Pro	Asp	Tyr	Gly	Lys	Arg	Phe	Ser	Ser	Glu
				725					730					735	
Ile	Thr	His	Lys	Asp	Val	Val	Gln	Gln	Asn	Asn	Thr	Leu	Ile	Glu	Glu
			740					745					750		
Met	Leu	Tyr	Leu	Ile	Ile	Met	Leu	Val	Gly	Glu	Arg	Phe	Ser	Pro	Gly
		755					760					765			
Val	Gly	Gln	Val	Asn	Ala	Thr	Asp	Glu	Ile	Lys	Arg	Glu	Ile	Ile	His
	770					775					780				
Gln	Leu	Ser	Ile	Lys	Pro	Met	Ala	His	Ser	Glu	Leu	Val	Lys	Ser	Leu
785					790					795					800
Pro	Glu	Asp	Glu	Asn	Lys	Glu	Thr	Gly	Met	Glu	Ser	Val	Ile	Glu	Ala
				805					810					815	
Val	Ala	His	Phe	Lys	Lys	Pro	Gly	Leu	Thr	Gly	Arg	Gly	Met	Tyr	Glu
			820					825					830		
Leu	Lys	Pro	Glu	Cys	Ala	Lys	Glu	Phe	Asn	Leu	Tyr	Phe	Tyr	His	Phe
		835					840					845			
Ser	Arg	Ala	Glu	Gln	Ser	Lys	Ala	Glu	Glu	Ala	Gln	Arg	Lys	Leu	Lys
	850					855					860				
Arg	Gln	Asn	Arg	Glu	Asp	Thr	Ala	Leu	Pro	Pro	Pro	Val	Leu	Pro	Pro
865					870					875					880
Phe	Cys	Pro	Leu	Phe	Ala	Ser	Leu	Val	Asn	Ile	Leu	Gln	Ser	Asp	Val
				885					890					895	
Met	Leu	Cys	Ile	Met	Gly	Thr	Ile	Leu	Gln	Trp	Ala	Val	Glu	His	Asn
			900					905					910		
Gly	Tyr	Ala	Trp	Ser	Glu	Ser	Met	Leu	Gln	Arg	Val	Leu	His	Leu	Ile
		915					920					925			
Gly	Met	Ala	Leu	Gln	Glu	Glu	Lys	Gln	His	Leu	Glu	Asn	Val	Thr	Glu
	930					935						940			
Glu	His	Val	Val	Thr	Phe	Thr	Phe	Thr	Gln	Lys	Ile	Ser	Lys	Pro	Gly
945					950					955					960
Glu	Ala	Pro	Lys	Asn	Ser	Pro	Ser	Ile	Leu	Ala	Met	Leu	Glu	Thr	Leu
				965					970					975	
Gln	Asn	Ala	Pro	Tyr	Leu	Glu	Val	His	Lys	Asp	Met	Ile	Arg	Trp	Ile
				980				985					990		
Leu	Lys	Thr	Phe	Asn	Ala	Val	Lys	Lys	Met	Arg	Glu	Ser	Ser	Pro	Thr
				995			1000					1005			

1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030 2035 2040 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400 2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490 2495 2500 2505 2510 2515 2520 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580 2585 2590 2595 2600 2605 2610 2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790 2795 2800 2805 2810 2815 2820 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880 2885 2890 2895 2900 2905 2910 2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420 3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480 3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540 3545 3550 3555 3560 3565 3570 3575 3580 3585 3590 3595 3600 3605 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660 3665 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770 3775 3780 3785 3790 3795 3800 3805 3810 3815 3820 3825 3830 3835 3840 3845 3850 3855 3860 3865 3870 3875 3880 3885 3890 3895 3900 3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000 4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095 4100 4105 4110 4115 4120 4125 4130 4135 4140 4145 4150 4155 4160 4165 4170 4175 4180 4185 4190 4195 4200 4205 4210 4215 4220 4225 4230 4235 4240 4245 4250 4255 4260 4265 4270 4275 4280 4285 4290 4295 4300 4305 4310 4315 4320 4325 4330 4335 4340 4345 4350 4355 4360 4365 4370 4375 4380 4385 4390 4395 4400 4405 4410 4415 4420 4425 4430 4435 4440 4445 4450 4455 4460 4465 4470 4475 4480 4485 4490 4495 4500 4505 4510 4515 4520 4525 4530 4535 4540 4545 4550 4555 4560 4565 4570 4575 4580 4585 4590 4595 4600 4605 4610 4615 4620 4625 4630 4635 4640 4645 4650 4655 4660 4665 4670 4675 4680 4685 4690 4695 4700 4705 4710 4715 4720 4725 4730 4735 4740 4745 4750 4755 4760 4765 4770 4775 4780 4785 4790 4795 4800 4805 4810 4815 4820 4825 4830 4835 4840 4845 4850 4855 4860 4865 4870 4875 4880 4885 4890 4895 4900 4905 4910 4915 4920 4925 4930 4935 4940 4945 4950 4955 4960 4965 4970 4975 4980 4985 4990 4995 5000 5005 5010 5015 5020 5025 5030 5035 5040 5045 5050 5055 5060 5065 5070 5075 5080 5085 5090 5095 5100 5105 5110 5115 5120 5125 5130 5135 5140 5145 5150 5155 5160 5165 5170 5175 5180 5185 5190 5195 5200 5205 5210 5215 5220 5225 5230 5235 5240 5245 5250 5255 5260 5265 5270 5275 5280 5285 5290 5295 5300 5305 5310 5315 5320 5325 5330 5335 5340 5345 5350 5355 5360 5365 5370 5375 5380 5385 5390 5395 5400 5405 5410 5415 5420 5425 5430 5435 5440 5445 5450 5455 5460 5465 5470 5475 5480 5485 5490 5495 5500 5505 5510 5515 5520 5525 5530 5535 5540 5545 5550 5555 5560 5565 5570 5575 5580 5585 5590 5595 5600 5605 5610 5615 5620 5625 5630 5635 5640 5645 5650 5655 5660 5665 5670 5675 5680 5685 5690 5695 5700 5705 5710 5715 5720 5725 5730 5735 5740 5745 5750 5755 5760 5765 5770 5775 5780 5785 5790 5795 5800 5805 5810 5815 5820 5825 5830 5835 5840 5845 5850 5855 5860 5865 5870 5875 5880 5885 5890 5895 5900 5905 5910 5915 5920 5925 5930 5935 5940 5945 5950 5955 5960 5965 5970 5975 5980 5985 5990 5995 6000 6005 6010 6015 6020 6025 6030 6035 6040 6045 6050 6055 6060 6065 6070 6075 6080 6085 6090 6095 6100 6105 6110 6115 6120 6125 6130 6135 6140 6145 6150 6155 6160 6165 6170 6175 6180 6185 6190 6195 6200 6205 6210 6215 6220 6225 6230 6235 6240 6245 6250 6255 6260 6265 6270 6275 6280 6285 6290 6295 6300 6305 6310 6315 6320 6325 6330 6335 6340 6345 6350 6355 6360 6365 6370 6375 6380 6385 6390 6395 6400 6405 6410 6415 6420 6425 6430 6435 6440 6445 6450 6455 6460 6465 6470 6475 6480 6485 6490 6495 6500 6505 6510 6515 6520 6525 6530 6535 6540 6545 6550 6555 6560 6565 6570 6575 6580 6585 6590 6595 6600 6605 6610 6615 6620 6625 6630 6635 6640 6645 6650 6655 6660 6665 6670 6675 6680 6685 6690 6695 6700 6705 6710 6715 6720 6725 6730 6735 6740 6745 6750 6755 6760 6765 6770 6775 6780 6785 6790 6795 6800 6805 6810 6815 6820 6825 6830 6835 6840 6845 6850 6855 6860 6865 6870 6875 6880 6885 6890 6895 6900 6905 6910 6915 6920 6925 6930 6935 6940 6945 6950 6955 6960 6965 6970 6975 6980 6985 6990 6995 7000 7005 7010 7015 7020 7025 7030 7035 7040 7045 7050 7055 7060 7065 7070 7075 7080 7085 7090 7095 7100 7105 7110 7115 7120 7125 7130 7135 7140 7145 7150 7155 7160 7165 7170 7175 7180 7185 7190 7195 7200 7205 7210 7215 7220 7225 7230 7235 7240 7245 7250 7255 7260 7265 7270 7275 7280 7285 7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400 7405 7410 7415 7420 7425 7430 7435 7440 7445 7450 7455 7460 7465 7470 7475 7480 7485 7490 7495 7500 7505 7510 7515 7520 7525 7530 7535 7540 7545 7550 7555 7560 7565 7570 7575 7580 7585 7590 7595 7600 7605 7610 7615 7620 7625 7630 7635 7640 7645 7650 7655 7660 7665 7670 7675 7680 7685 7690 7695 7700 7705 7710 7715 7720 7725 7730 7735 7740 7745 7750 7755 7760 7765 7770 7775 7780 7785 7790 7795 7800 7805 7810 7815 7820 7825 7830 7835 7840 7845 7850 7855 7860 7865 7870 7875 7880 7885 7890 7895 7900 7905 7910 7915 7920 7925 7930 7935 7940 7945 7950 7955 7960 7965 7970 7975 7980 7985 7990 7995 8000 8005 8010 8015 8020 8025 8030 8035 8040 8045 8050 8055 8060 8065 8070 8075 8080 8085 8090 8095 8100 8105 8110 8115 8120 8125 8130 8135 8140 8145 8150 8155 8160 8165 8170 8175 8180 8185 8190 8195 8200 8205 8210 8215 8220 8225 8230 8235 8240 8245 8250 8255 8260 8265 8270 8275 8280 8285 8290 8295 8300 8305 8310 8315 8320 8325 8330 8335 8340 8345 8350 8355 8360 8365 8370 8375 8380 8385 8390 8395 8400 8405 8410 8415 8420 8425 8430 8435 8440 8445 8450 8455 8460 8465 8470 8475 8480 8485 8490 8495 8500 8505 8510 8515 8520 8525 8530 8535 8540 8545 8550 8555 8560 8565 8570 8575 8580 8585 8590 8595 8600 8605 8610 8615 8620 8625 8630 8635 8640 8645 8650 8655 8660 8665 8670 8675 8680 8685 8690 8695 8700 8705 8710 8715 8720 8725 8730 8735 8740 8745 8750 8755 8760 8765 8770 8775 8780 8785 8790 8795 8800 8805 8810 8815 8820 8825 8830 8835 8840 8845 8850 8855 8860 8865 8870 8875 8880 8885 8890 8895 8900 8905 8910 8915 8920 8925 8930 8935 8940 8945 8950 8955 8960 8965 8970 8975 8980 8985 8990 8995 9000 9005 9010 9015 9020 9025 9030 9035 9040 9045 9050 9055 9060 9065 9070 9075 9080 9085 9090 9095 9100 9105 9110 9115 9120 9125 9130 9135 9140 9145 9150 9155 9160 9165 9170 9175 9180 9185 9190 9195 9200 9205 9210 9215 9220 9

Ser Pro Val Ala Glu Thr Glu Gly Thr Ile Met Glu Glu Ser Ser Arg
1010 1015 1020

Asp Lys Asp Lys Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu
025 1030 1035 1040

Arg Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe
1045 1050 1055

Ile Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Ala
1060 1065 1070

Ser Thr Ser Ala Val Leu Asp His Ser Pro Val Ala Ser Asp Met Thr
1075 1080 1085

Leu Thr Ala Leu Gly Pro Thr Gln Thr Gln Val Pro Glu Gln Arg Gln
1090 1095 1100

Phe Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Lys Val Glu
1105 1110 1115 1120

Ser Arg Ala Met Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu
1125 1130 1135

Ser Lys Asn Arg Ser Lys Phe Ile Gln Asp Pro Glu Lys Tyr Asp Pro
1140 1145 1150

Leu Phe Met His Pro Asp Leu Ser Cys Gly Thr His Thr Ser Ser Cys
1155 1160 1165

Gly His Ile Met His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val
1170 1175 1180

Gln Ala Lys Glu Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser
1185 1190 1195 1200

Tyr Asp Val Glu Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu
1205 1210 1215

Ser Asn Thr Val Ile Pro Leu Leu Leu Pro Pro Arg Asn Ile Phe Asn
1220 1225 1230

Asn Arg Leu Asn Phe Ser Asp Gln Pro Asn Leu Thr Gln Trp Ile Arg
1235 1240 1245

Thr Ile Ser Gln Gln Ile Lys Ala Leu Gln Phe Leu Arg Lys Glu Glu
1250 1255 1260

Ser Thr Pro Asn Asn Ala Ser Thr Lys Asn Ser Glu Asn Val Asp Glu
1265 1270 1275 1280

Leu Gln Leu Pro Glu Gly Phe Arg Pro Asp Phe Arg Pro Lys Ile Pro
1285 1290 1295

Tyr Ser Glu Ser Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Thr
1300 1305 1310

Tyr Lys Val Gly Leu Lys Val His Pro Asn Glu Glu Asp Pro Arg Val
1315 1320 1325

Pro Ile Met Cys Trp Gly Ser Cys Ala Tyr Thr Ile Gln Ser Ile Glu
1330 1335 1340

Ser Cys Gly Ser Gly Val Gly Ile Phe Leu Arg Val Arg Glu Cys Gln
665 1670 1675 1680

Val Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro
1685 1690 1695

Tyr Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn
1700 1705 1710

Pro Leu His Leu Cys Lys Glu Arg Phe Lys Lys Ile Gln Lys Leu Trp
1715 1720 1725

His Gln His Ser Val Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn
1730 1735 1740

Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu
745 1750 1755

<210> 5
<211> 6089
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (766) .. (6030)

<400> 5
caagtgtatc atatgccaaag tacgccccct attgacgtca atgacggtaa atggcccgcc 60
tggcattatg cccagtacat gaccttatgg gactttccta cttggcagta catctacgta 120
ttagtcatcg ctattaccat ggtgatgcgg ttttggcagt acatcaatgg gcgtggatag 180
cggtttgact cacgggggatt tccaagtctc caccgccattg acgtcaatgg gagtttgttt 240
tggcaccaaa atcaacggga ctttccaaaa tgctgtaaca actccgcccc attgacgcaa 300
atggggcggtg ggogtgtacg gtgggaggtc tatataagca gagctctctg gctaactaga 360
gaaccactg cttactggct tatcgaaatt aatacgactc actataggga gacccaagct 420
tggtaccgag ctggatcca ctactcgacc cacgcgtccg cggtagtggc tgtccggagt 480
gccaggcctg gggttctcgg tgctcttccc ccggtcacgg gcgaggaggc gacttgactt 540
ctgggcgcgg agcccgggcg cgcgcgcaag cggtgcccgt ccccgctgca ggttcgcgtc 600
ccgctttgct cctcgcgcac ctcggtctcg cggcagcccc gacggccccg gactgacggc 660
cccaggacag gggtgaccgt cgcggctgcg ggagcagagg cgaagctgag gcccggggag 720
aggcgacagc ggcgagagca cccggggaga ggaggaggag agaag atg gcg tcg gag 777
Met Ala Ser Glu

1

atg gag ccc gag gtg cag gcc atc gac cgc agt ttg ctg gaa tgt tct 825
Met Glu Pro Glu Val Gln Ala Ile Asp Arg Ser Leu Leu Glu Cys Ser
5 10 15 20

gcc gaa gag atc gca ggg aga tgg ctg caa gca acc gac ctc aac aga 873
Ala Glu Glu Ile Ala Gly Arg Trp Leu Gln Ala Thr Asp Leu Asn Arg
25 30 35

gaa Glu	gtg Val	tac Tyr	cag Gln 40	cat His	tta Leu	gcc Ala	cac His	tgt Cys 45	gtg Val	ccc Pro	aaa Lys	atc Ile	tac Tyr 50	tgc Cys	cgg Arg	921
ggc Gly	cct Pro	aac Asn 55	ccc Pro	ttc Phe	cct Pro	cag Gln	aag Lys 60	gaa Glu	gac Asp	acg Thr	ctg Leu 65	gca Ala	cag Gln	cac His	atc Ile	969
ctg Leu 70	ctg Leu	gga Gly	ccg Pro	atg Met	gag Glu	tgg Trp 75	tac Tyr	atc Ile	tgc Cys	gct Ala 80	gaa Glu	gac Asp	cct Pro	gcg Ala	ctg Leu	1017
gga Gly 85	ttt Phe	cca Pro	aag Lys	ctc Leu 90	gag Glu	cag Gln	gca Ala	aac Asn	aag Lys	cct Pro 95	tct Ser	cac His	ctc Leu	tgt Cys	ggc Gly 100	1065
cga Arg	gtg Val	ttt Phe	aaa Lys	gtg Val 105	ggg Gly	gaa Glu	cct Pro	aca Thr	tac Tyr 110	tcc Ser	tgc Cys	aga Arg	gac Asp	tgt Cys 115	gca Ala	1113
gtt Val	gac Asp	ccc Pro	acc Thr 120	tgt Cys	gtt Val	tta Leu	tgc Cys	atg Met 125	gag Glu	tgc Cys	ttc Phe	ctg Leu 130	gga Gly	agt Ser	atc Ile	1161
cat His	aga Arg	gac Asp 135	cat His	cga Arg	tat Tyr	agg Arg	atg Met 140	acc Thr	aca Thr	tcg Ser	gga Gly 145	gga Gly	ggg Gly	ggc Gly	ttc Phe	1209
tgt Cys	gac Asp 150	tgt Cys	ggt Gly	gac Asp	act Thr	gag Glu 155	gcg Ala	tgg Trp	aaa Lys	gag Glu 160	gga Gly	cct Pro	tac Tyr	tgc Cys	cag Gln	1257
aag Lys 165	cac His	aag Lys	ctc Leu	agc Ser	agc Ser 170	tct Ser	gaa Glu	gtt Val	gtg Val	gag Glu 175	gag Glu	gag Glu	gat Asp	cct Pro	ctt Leu 180	1305
gtg Val	cat His	cta Leu	tca Ser 185	gaa Glu	gat Asp	gtg Val	atc Ile	gcc Ala 190	aga Arg	act Thr	tac Tyr	aac Asn	att Ile 195	ttt Phe	gct Ala	1353
att Ile	atg Met	ttt Phe 200	cga Arg	tat Tyr	gca Ala	gta Val	gat Asp	ata Ile 205	ctg Leu	acc Thr	tgg Trp	gaa Glu 210	aaa Lys	gaa Glu	agt Ser	1401
gaa Glu	ttg Leu 215	cct Pro	gaa Glu	gac Asp	tta Leu	gaa Glu	gtg Val 220	gca Ala	gag Glu	aag Lys	agt Ser 225	gac Asp	acc Thr	tac Tyr	tac Tyr	1449
tgc Cys	atg Met 230	ctg Leu	ttt Phe	aat Asn	gat Asp	gag Glu 235	gtt Val	cac His	acc Thr	tat Tyr	gag Glu 240	caa Gln	gtc Val	att Ile	tat Tyr	1497
acc Thr 245	ctt Leu	cag Gln	aaa Lys	gct Ala 250	gtg Val	aac Asn	tgt Cys	aca Thr	cag Gln	aag Lys 255	gaa Glu	gcc Ala	att Ile	ggc Gly	ttt Phe 260	1545
gca Ala	act Thr	aca Thr	gtt Val	gat Asp 265	cga Arg	gat Asp	ggc Gly	cgt Arg	agg Arg 270	cct Pro	gtc Val	cga Arg	tat Tyr	gga Gly 275	gat Asp	1593
ttc Phe	cag Gln	tac Tyr	tgt Cys 280	gat Asp	caa Gln	gca Ala	aag Lys	aca Thr 285	gtc Val	att Ile	gtg Val	agg Arg	aac Asn 290	acc Thr	agc Ser	1641

aga	cag	acc	aag	ccg	ctc	aaa	gtt	caa	gtt	atg	cac	tcc	tcc	gtg	gct	1689
Arg	Gln	Thr	Lys	Pro	Leu	Lys	Val	Gln	Val	Met	His	Ser	Ser	Val	Ala	
		295					300					305				
gct	cat	cag	aat	ttt	ggg	ttg	aaa	gct	ctg	tcg	tgg	ctg	gga	agt	gtt	1737
Ala	His	Gln	Asn	Phe	Gly	Leu	Lys	Ala	Leu	Ser	Trp	Leu	Gly	Ser	Val	
	310					315					320					
att	gga	tac	tca	gat	ggc	ctt	cgc	agg	att	ttg	tgt	caa	gtt	gga	tta	1785
Ile	Gly	Tyr	Ser	Asp	Gly	Leu	Arg	Arg	Ile	Leu	Cys	Gln	Val	Gly	Leu	
325					330					335					340	
caa	gaa	ggg	cca	gat	ggc	gaa	aac	tct	tct	ctg	gtc	gac	aga	ctg	atg	1833
Gln	Glu	Gly	Pro	Asp	Gly	Glu	Asn	Ser	Ser	Leu	Val	Asp	Arg	Leu	Met	
				345					350					355		
ctt	aat	gat	tcc	aaa	tta	tgg	aaa	ggg	gct	agg	agt	gtg	tat	cac	cag	1881
Leu	Asn	Asp	Ser	Lys	Leu	Trp	Lys	Gly	Ala	Arg	Ser	Val	Tyr	His	Gln	
			360					365					370			
ttg	ttc	atg	agc	agc	ctg	ctc	atg	gac	ctc	aag	tat	aag	aag	ctg	ttc	1929
Leu	Phe	Met	Ser	Ser	Leu	Leu	Met	Asp	Leu	Lys	Tyr	Lys	Lys	Leu	Phe	
		375					380					385				
gcg	ctt	cga	ttt	gct	aaa	aat	tac	cgg	cag	ttg	cag	agg	gat	ttt	atg	1977
Ala	Leu	Arg	Phe	Ala	Lys	Asn	Tyr	Arg	Gln	Leu	Gln	Arg	Asp	Phe	Met	
	390					395					400					
gag	gat	gat	cac	gag	cgg	gca	gtg	tcg	gtg	act	gct	ctg	tct	gtc	cag	2025
Glu	Asp	Asp	His	Glu	Arg	Ala	Val	Ser	Val	Thr	Ala	Leu	Ser	Val	Gln	
405					410					415					420	
ttc	ttc	acc	gca	ccg	acg	ctg	gcg	cga	atg	ctc	ctc	aca	gaa	gag	aac	2073
Phe	Phe	Thr	Ala	Pro	Thr	Leu	Ala	Arg	Met	Leu	Leu	Thr	Glu	Glu	Asn	
			425					430						435		
ctg	atg	acc	gtt	atc	att	aag	gct	ttc	atg	gac	cat	ttg	aaa	cac	aga	2121
Leu	Met	Thr	Val	Ile	Ile	Lys	Ala	Phe	Met	Asp	His	Leu	Lys	His	Arg	
			440					445					450			
gat	gcc	cag	ggc	aga	ttc	cag	ttt	gaa	cgc	tac	act	gcc	ctc	caa	gcc	2169
Asp	Ala	Gln	Gly	Arg	Phe	Gln	Phe	Glu	Arg	Tyr	Thr	Ala	Leu	Gln	Ala	
		455				460						465				
ttc	aag	ttc	agg	aga	gtc	cag	agc	ctc	atc	tta	gat	ctc	aag	tat	gta	2217
Phe	Lys	Phe	Arg	Arg	Val	Gln	Ser	Leu	Ile	Leu	Asp	Leu	Lys	Tyr	Val	
	470					475					480					
ttg	att	agc	aaa	cca	acg	gag	tgg	tca	gat	gag	ctg	agg	cag	aag	ttc	2265
Leu	Ile	Ser	Lys	Pro	Thr	Glu	Trp	Ser	Asp	Glu	Leu	Arg	Gln	Lys	Phe	
485					490					495					500	
tta	caa	ggg	ttc	gat	gcc	ttc	ttg	gaa	tta	ctg	aag	tgc	atg	cag	gga	2313
Leu	Gln	Gly	Phe	Asp	Ala	Phe	Leu	Glu	Leu	Leu	Lys	Cys	Met	Gln	Gly	
				505					510					515		
atg	gac	ccg	atc	acg	cgt	cag	gtg	gga	cag	cac	att	gag	atg	gag	cca	2361
Met	Asp	Pro	Ile	Thr	Arg	Gln	Val	Gly	Gln	His	Ile	Glu	Met	Glu	Pro	
			520					525					530			
gag	tgg	gaa	gca	gcc	ttc	aca	ctg	cag	atg	aag	ctg	aca	cac	gtc	atc	2409
Glu	Trp	Glu	Ala	Ala	Phe	Thr	Leu	Gln	Met	Lys	Leu	Thr	His	Val	Ile	
		535					540						545			

tca atg gtg cag gac tgg tgt gct ctg gac gaa aaa gtg tta att gaa	2457
Ser Met Val Gln Asp Trp Cys Ala Leu Asp Glu Lys Val Leu Ile Glu	
550 555 560	
gct tac aag aaa tgc ctg gct gtg ctg aca cag tgt cat ggc gga ttt	2505
Ala Tyr Lys Lys Cys Leu Ala Val Leu Thr Gln Cys His Gly Gly Phe	
565 570 575 580	
act gat ggt gaa cag cca atc aca ctc agt att tgt gga cac tcg gtg	2553
Thr Asp Gly Glu Gln Pro Ile Thr Leu Ser Ile Cys Gly His Ser Val	
585 590 595	
gaa acc atc aga tac tgt gtt tcc caa gaa aaa gtt agc att cac ctc	2601
Glu Thr Ile Arg Tyr Cys Val Ser Gln Glu Lys Val Ser Ile His Leu	
600 605 610	
cca att tct cgc ttg ctt gca ggt ttg cat gta ttg tta agc aaa agt	2649
Pro Ile Ser Arg Leu Leu Ala Gly Leu His Val Leu Ser Lys Ser	
615 620 625	
gaa gtg gca tat aaa ttt cca gag ctc cta cct cta agt gaa ctg agc	2697
Glu Val Ala Tyr Lys Phe Pro Glu Leu Leu Pro Leu Ser Glu Leu Ser	
630 635 640	
cca ccc atg ttg ata gaa cat cct ctt aga tgt ctt gtc tta tgt gct	2745
Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu Val Leu Cys Ala	
645 650 655 660	
caa gtg cat gct ggg atg tgg aga aga aat ggc ttc tct cta gta aat	2793
Gln Val His Ala Gly Met Trp Arg Arg Asn Gly Phe Ser Leu Val Asn	
665 670 675	
cag atc tat tac tac cat aat gtg aaa tgc agg cga gag atg ttc gac	2841
Gln Ile Tyr Tyr Tyr His Asn Val Lys Cys Arg Arg Glu Met Phe Asp	
680 685 690	
aag gac ata gtg atg ctt cag aca ggt gtc tcc atg atg gac cca aac	2889
Lys Asp Ile Val Met Leu Gln Thr Gly Val Ser Met Met Asp Pro Asn	
695 700 705	
cac ttc ctg atg atc atg ctc agc cgc ttt gaa ctc tat cag ctc ttc	2937
His Phe Leu Met Ile Met Leu Ser Arg Phe Glu Leu Tyr Gln Leu Phe	
710 715 720	
agc acg cct gac tat ggg aag aga ttc agt tct gag gtt acc cat aag	2985
Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu Val Thr His Lys	
725 730 735 740	
gac gtc gtt cag cag aac aac act ctg atc gaa gag atg ctc tac ctc	3033
Asp Val Val Gln Gln Asn Asn Thr Leu Ile Glu Glu Met Leu Tyr Leu	
745 750 755	
atc atc atg ctt gtg gga gaa aga ttc aac cct ggg gtt gga cag gtg	3081
Ile Ile Met Leu Val Gly Glu Arg Phe Asn Pro Gly Val Gly Gln Val	
760 765 770	
gct gcc aca gat gaa atc aag agg gag att atc cat cag ttg agc atc	3129
Ala Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His Gln Leu Ser Ile	
775 780 785	
aag cct atg gct cac agt gag ctg gtg aag tct ctg cct gaa gat gag	3177
Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu Pro Glu Asp Glu	
790 795 800	

aac aag gag acc ggc atg gag agc gtc atc gag tcc gtt gca cat ttc	3225
Asn Lys Glu Thr Gly Met Glu Ser Val Ile Glu Ser Val Ala His Phe	
805 810 815 820	
aag aaa cct ggg ctc aca ggg cga ggc atg tat gag ctg aag cca gag	3273
Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu Leu Lys Pro Glu	
825 830 835	
tgt gcc aaa gag ttc aac ctg tat ttt tat cat ttc tcc agg gca gag	3321
Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe Ser Arg Ala Glu	
840 845 850	
cag tcc aag gca gag gaa gct cag cgg aaa ttg aaa aga gaa aat aaa	3369
Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys Arg Glu Asn Lys	
855 860 865	
gaa gat aca gca ctc cct cct ccg gct ttg cca ccg ttc tgc cct ttg	3417
Glu Asp Thr Ala Leu Pro Pro Ala Leu Pro Phe Cys Pro Leu	
870 875 880	
ttc gcg agt ctg gtt aac atc ttg cag tgt gac gtc atg ctg tac atc	3465
Phe Ala Ser Leu Val Asn Ile Leu Gln Cys Asp Val Met Leu Tyr Ile	
885 890 895 900	
atg gga acg atc ctg cag tgg gct gta gag cat cac ggg tct gcc tgg	3513
Met Gly Thr Ile Leu Gln Trp Ala Val Glu His His Gly Ser Ala Trp	
905 910 915	
tca gag tcc atg cta cag agg gtg ctg cat ttg atc ggg atg gct ctc	3561
Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile Gly Met Ala Leu	
920 925 930	
cag gaa gag aag cac cac ttg gag aac gcc gtg gaa ggg cac gtg cag	3609
Gln Glu Glu Lys His His Leu Glu Asn Ala Val Glu Gly His Val Gln	
935 940 945	
acc ttc acc ttc aca cag aag att tca aag cct ggt gat gca cca cat	3657
Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly Asp Ala Pro His	
950 955 960	
aac tcc ccg agc atc cta gct atg ctg gag acc ttg cag aac gcc ccc	3705
Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu Gln Asn Ala Pro	
965 970 975 980	
tcc ctg gaa gcc cac aag gac atg atc agg tgg ttg cta aag atg ttt	3753
Ser Leu Glu Ala His Lys Asp Met Ile Arg Trp Leu Leu Lys Met Phe	
985 990 995	
aat gca att aag aag ata aga gag tgt tca tcc agc agc cct gtg gcc	3801
Asn Ala Ile Lys Lys Ile Arg Glu Cys Ser Ser Ser Ser Pro Val Ala	
1000 1005 1010	
gag gcg gag gga acc ata atg gag gag agc tca aga gac aag gac aaa	3849
Glu Ala Glu Gly Thr Ile Met Glu Glu Ser Ser Arg Asp Lys Asp Lys	
1015 1020 1025	
gca gag agg aaa aga aaa gcc gag atc gcc aga ctg cgc cgg gag aag	3897
Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu Arg Arg Glu Lys	
1030 1035 1040	
atc atg gcc cag atg tct gag atg cag cgg cac ttc att gac gaa aac	3945
Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe Ile Asp Glu Asn	
1045 1050 1055 1060	

aaa Lys	gag Glu	ctc Leu	ttc Phe	cag Gln	cag Gln	acc Thr	cta Leu	gag Glu	ctg Leu	gac Asp	acc Thr	tct Ser	gcc Ala	tct Ser	gcc Ala	3993
			1065						1070			1075				
act Thr	ctt Leu	gac Asp	agc Ser	agc Ser	cct Pro	ccc Pro	gtt Val	tca Ser	gac Asp	gca Ala	gct Ala	ctt Leu	aca Thr	gca Ala	ctg Leu	4041
			1080						1085			1090				
ggc Gly	cca Pro	gca Ala	cag Gln	aca Thr	cag Gln	gtc Val	cct Pro	gaa Glu	ccg Pro	aga Arg	cag Gln	ttt Phe	gtc Val	acc Thr	tgt Cys	4089
			1095						1100			1105				
ata Ile	tta Leu	tgt Cys	caa Gln	gag Glu	gag Glu	caa Gln	gag Glu	gtg Val	act Thr	gtg Val	gga Gly	agc Ser	agg Arg	gcg Ala	atg Met	4137
			1110						1115			1120				
gtc Val	ttg Leu	gca Ala	gcg Ala	ttt Phe	gtt Val	cag Gln	agg Arg	tca Ser	acg Thr	gtt Val	ctg Leu	tca Ser	aaa Lys	gac Asp	agg Arg	4185
			1125						1130			1135			1140	
acg Thr	aaa Lys	acc Thr	atc Ile	gcg Ala	gac Asp	cca Pro	gaa Glu	aaa Lys	tat Tyr	gat Asp	cca Pro	tta Leu	ttc Phe	atg Met	cac His	4233
			1145						1150			1155				
ccc Pro	gat Asp	ctg Leu	tct Ser	tgt Cys	ggg Gly	aca Thr	cac His	act Thr	ggc Gly	agc Ser	tgt Cys	ggg Gly	cac His	gtt Val	atg Met	4281
			1160						1165			1170				
cat His	gcc Ala	cat His	tgt Cys	tgg Trp	caa Gln	agg Arg	tat Tyr	ttt Phe	gat Asp	tcc Ser	gtt Val	caa Gln	gcc Ala	aag Lys	gag Glu	4329
			1175						1180			1185				
cag Gln	cga Arg	agg Arg	cag Gln	cag Gln	cgg Arg	ctg Leu	cgc Arg	ttg Leu	cac His	act Thr	agc Ser	tac Tyr	gat Asp	gta Val	gag Glu	4377
			1190						1195			1200				
aat Asn	ggc Gly	gag Glu	ttc Phe	ctc Leu	tgc Cys	ccg Pro	ctc Leu	tgt Cys	gag Glu	tgc Cys	ctg Leu	agc Ser	aac Asn	acg Thr	gtg Val	4425
			1205						1210			1215			1220	
atc Ile	ccc Pro	ctg Leu	ctg Leu	ctt Leu	cct Pro	ccc Pro	agg Arg	agc Ser	atc Ile	ctc Leu	agc Ser	agg Arg	agg Arg	tta Leu	aat Asn	4473
			1225						1230			1235				
ttt Phe	tca Ser	gac Asp	caa Gln	cca Pro	gat Asp	ctg Leu	gca Ala	cag Gln	tgg Trp	acg Thr	aga Arg	gca Ala	gta Val	aca Thr	cag Gln	4521
			1240						1245			1250				
cag Gln	ata Ile	aag Lys	gtg Val	gtc Val	cag Gln	atg Met	ctg Leu	agg Arg	aga Arg	aag Lys	cac His	aat Asn	gct Ala	gct Ala	gac Asp	4569
			1255						1260			1265				
acg Thr	tct Ser	tct Ser	tca Ser	gag Glu	gac Asp	aca Thr	gaa Glu	gcc Ala	atg Met	aat Asn	ata Ile	ata Ile	ccg Pro	atc Ile	ccc Pro	4617
			1270						1275			1280				
gaa Glu	ggc Gly	ttc Phe	agg Arg	cct Pro	gat Asp	ttt Phe	tat Tyr	cct Pro	agg Arg	aac Asn	cca Pro	tat Tyr	tct Ser	gat Asp	agc Ser	4665
			1285						1290			1295			1300	
ata Ile	aaa Lys	gaa Glu	atg Met	tta Leu	acg Thr	aca Thr	ttt Phe	gga Gly	acg Thr	gct Ala	gct Ala	tac Tyr	aag Lys	gtg Val	gga Gly	4713
			1305						1310			1315				

ctg	aag	ggt	cat	cct	aat	gaa	ggg	gac	ccc	cgt	gtg	ccc	atc	ctg	tgc	4761
Leu	Lys	Val	His	Pro	Asn	Glu	Gly	Asp	Pro	Arg	Val	Pro	Ile	Leu	Cys	
			1320				1325						1330			
tgg	ggg	acc	tgt	gca	tac	acc	atc	cag	agc	ata	gaa	aga	att	ttg	agt	4809
Trp	Gly	Thr	Cys	Ala	Tyr	Thr	Ile	Gln	Ser	Ile	Glu	Arg	Ile	Leu	Ser	
			1335				1340						1345			
gat	gag	gag	aag	cct	gtt	ttt	gga	cct	ctg	cct	tgt	aga	ctg	gac	gac	4857
Asp	Glu	Glu	Lys	Pro	Val	Phe	Gly	Pro	Leu	Pro	Cys	Arg	Leu	Asp	Asp	
			1350				1355						1360			
tgt	ctc	agg	tcg	tta	aca	cgg	ttt	gca	gca	gca	cat	tgg	aca	gtg	gcg	4905
Cys	Leu	Arg	Ser	Leu	Thr	Arg	Phe	Ala	Ala	Ala	His	Trp	Thr	Val	Ala	
			1365				1370						1380			
tta	ctt	cct	gtg	gta	caa	gga	cac	ttc	tgt	aaa	ctc	ttt	gca	tcc	ttg	4953
Leu	Leu	Pro	Val	Val	Gln	Gly	His	Phe	Cys	Lys	Leu	Phe	Ala	Ser	Leu	
			1385				1390						1395			
gtg	cct	agt	gac	agc	tat	gaa	gac	ctc	ccg	tgc	ata	cta	gac	atc	gac	5001
Val	Pro	Ser	Asp	Ser	Tyr	Glu	Asp	Leu	Pro	Cys	Ile	Leu	Asp	Ile	Asp	
			1400				1405						1410			
atg	ttt	cac	ttg	ctg	gtg	ggc	ctg	gtg	ctc	gct	ttc	cca	gct	ctg	cag	5049
Met	Phe	His	Leu	Leu	Val	Gly	Leu	Val	Leu	Ala	Phe	Pro	Ala	Leu	Gln	
			1415				1420						1425			
tgt	cag	gat	ttt	tca	gga	agc	agc	ctg	gcc	act	ggg	gac	ctg	cac	atc	5097
Cys	Gln	Asp	Phe	Ser	Gly	Ser	Ser	Leu	Ala	Thr	Gly	Asp	Leu	His	Ile	
			1430				1435						1440			
ttc	cac	ttg	ggt	acc	atg	gca	cac	atc	gta	cag	atc	tta	ctt	acc	tca	5145
Phe	His	Leu	Val	Thr	Met	Ala	His	Ile	Val	Gln	Ile	Leu	Leu	Thr	Ser	
			1445				1450						1460			
tgt	aca	gaa	gag	aat	ggc	atg	gat	caa	gag	aat	ccc	act	ggg	gaa	gaa	5193
Cys	Thr	Glu	Glu	Asn	Gly	Met	Asp	Gln	Glu	Asn	Pro	Thr	Gly	Glu	Glu	
			1465				1470						1475			
gaa	ctg	gcc	att	ctc	tct	ttg	cac	aaa	aca	ctt	cac	cag	tat	act	gga	5241
Glu	Leu	Ala	Ile	Leu	Ser	Leu	His	Lys	Thr	Leu	His	Gln	Tyr	Thr	Gly	
			1480				1485						1490			
agt	gcc	ttg	aaa	gaa	gcc	ccc	tcc	ggc	tgg	cac	ctg	tgg	agg	agc	gtc	5289
Ser	Ala	Leu	Lys	Glu	Ala	Pro	Ser	Gly	Trp	His	Leu	Trp	Arg	Ser	Val	
			1495				1500						1505			
cgg	gcc	gcc	atc	atg	cct	ttc	ctc	aag	tgc	tct	gct	ttg	ttt	ttc	cac	5337
Arg	Gla	Ala	Ile	Met	Pro	Phe	Leu	Lys	Cys	Ser	Ala	Leu	Phe	Phe	His	
			1510				1515						1520			
tat	tta	aat	gga	gtc	ccg	gcc	cct	cca	gac	ctt	caa	gtt	tct	gga	aca	5385
Tyr	Leu	Asn	Gly	Val	Pro	Ala	Pro	Pro	Asp	Leu	Gln	Val	Ser	Gly	Thr	
			1525				1530						1540			
agc	cat	ttt	gaa	cac	tta	tgt	aac	tac								

agt tgg tgc cag aac agt gaa gtt aaa cgg tat cta aat ggc gag aga 5529
 Ser Trp Cys Gln Asn Ser Glu Val Lys Arg Tyr Leu Asn Gly Glu Arg
 1575 1580 1585

 gga gcg ata agc tac ccc aga gga gct aac aaa ctg ata gac ctt cca 5577
 Gly Ala Ile Ser Tyr Pro Arg Gly Ala Asn Lys Leu Ile Asp Leu Pro
 1590 1595 1600

 gag gat tac agc agc ctc att aac caa gca tcc aat ttc tcg tgc ccc 5625
 Glu Asp Tyr Ser Ser Leu Ile Asn Gln Ala Ser Asn Phe Ser Cys Pro
 1605 1610 1615 1620

 aaa tca ggt ggc gac aag agc aga gct cct act ctg tgc ctc gtg tgt 5673
 Lys Ser Gly Gly Asp Lys Ser Arg Ala Pro Thr Leu Cys Leu Val Cys
 1625 1630 1635

 ggg agt ctc ctc tgc tct cag agt tac tgc tgc caa gct gag ctg gag 5721
 Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln Ala Glu Leu Glu
 1640 1645 1650

 ggt gag gac gtc gga gcc tgc aca gca cac acc tac tcc tgc ggc tcc 5769
 Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr Ser Cys Gly Ser
 1655 1660 1665

 ggg gcc ggc atc ttc ctg aga gtg cgg gaa tgt cag gtg cta ttt tta 5817
 Gly Ala Gly Ile Phe Leu Arg Val Arg Glu Cys Gln Val Leu Phe Leu
 1670 1675 1680

 gct ggc aaa acc aaa gga tgt ttt tat tct cct cct tac ctt gac gac 5865
 Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro Tyr Leu Asp Asp
 1685 1690 1695 1700

 tat gga gag acc gac cag gga ctc aga cga gga aat cct tta cat tta 5913
 Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn Pro Leu His Leu
 1705 1710 1715

 tgc caa gag cgg ttt cga aag atc cag aag ctc tgg cag cag cat agt 5961
 Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp Gln Gln His Ser
 1720 1725 1730

 atc aca gag gag atc gga cac gcg cag gag gct aac cag acc ctg gtc 6009
 Ile Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn Gln Thr Leu Val
 1735 1740 1745

 gga att gac tgg cag cat tta taatcgctcc tctactaaaa acttgacttg 6060
 Gly Ile Asp Trp Gln His Leu
 1750 1755

 gagtttttgta acacagctgg cttttccag 6089

<210> 6
 <211> 1755
 <212> PRT
 <213> Mouse

<400> 6
 Met Ala Ser Glu Met Glu Pro Glu Val Gln Ala Ile Asp Arg Ser Leu
 1 5 10 15
 Leu Glu Cys Ser Ala Glu Glu Ile Ala Gly Arg Trp Leu Gln Ala Thr
 20 25 30

Asp	Leu	Asn	Arg	Glu	Val	Tyr	Gln	His	Leu	Ala	His	Cys	Val	Pro	Lys
		35					40					45			
Ile	Tyr	Cys	Arg	Gly	Pro	Asn	Pro	Phe	Pro	Gln	Lys	Glu	Asp	Thr	Leu
	50					55					60				
Ala	Gln	His	Ile	Leu	Leu	Gly	Pro	Met	Glu	Trp	Tyr	Ile	Cys	Ala	Glu
65					70					75					80
Asp	Pro	Ala	Leu	Gly	Phe	Pro	Lys	Leu	Glu	Gln	Ala	Asn	Lys	Pro	Ser
				85					90					95	
His	Leu	Cys	Gly	Arg	Val	Phe	Lys	Val	Gly	Glu	Pro	Thr	Tyr	Ser	Cys
			100					105					110		
Arg	Asp	Cys	Ala	Val	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Glu	Cys	Phe
		115					120					125			
Leu	Gly	Ser	Ile	His	Arg	Asp	His	Arg	Tyr	Arg	Met	Thr	Thr	Ser	Gly
	130					135					140				
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Glu	Gly
145					150					155					160
Pro	Tyr	Cys	Gln	Lys	His	Lys	Leu	Ser	Ser	Ser	Glu	Val	Val	Glu	Glu
				165					170					175	
Glu	Asp	Pro	Leu	Val	His	Leu	Ser	Glu	Asp	Val	Ile	Ala	Arg	Thr	Tyr
			180					185					190		
Asn	Ile	Phe	Ala	Ile	Met	Phe	Arg	Tyr	Ala	Val	Asp	Ile	Leu	Thr	Trp
		195					200					205			
Glu	Lys	Glu	Ser	Glu	Leu	Pro	Glu	Asp	Leu	Glu	Val	Ala	Glu	Lys	Ser
	210					215					220				
Asp	Thr	Tyr	Tyr	Cys	Met	Leu	Phe	Asn	Asp	Glu	Val	His	Thr	Tyr	Glu
225					230					235					240
Gln	Val	Ile	Tyr	Thr	Leu	Gln	Lys	Ala	Val	Asn	Cys	Thr	Gln	Lys	Glu
				245					250					255	
Ala	Ile	Gly	Phe	Ala	Thr	Thr	Val	Asp	Arg	Asp	Gly	Arg	Arg	Pro	Val
			260					265					270		
Arg	Tyr	Gly	Asp	Phe	Gln	Tyr	Cys	Asp	Gln	Ala	Lys	Thr	Val	Ile	Val
		275					280					285			
Arg	Asn	Thr	Ser	Arg	Gln	Thr	Lys	Pro	Leu	Lys	Val	Gln	Val	Met	His
	290					295					300				
Ser	Ser	Val	Ala	Ala	His	Gln	Asn	Phe	Gly	Leu	Lys	Ala	Leu	Ser	Trp
305					310					315					320
Leu	Gly	Ser	Val	Ile	Gly	Tyr	Ser	Asp	Gly	Leu	Arg	Arg	Ile	Leu	Cys
				325					330					335	
Gln	Val	Gly	Leu	Gln	Glu	Gly	Pro	Asp	Gly	Glu	Asn	Ser	Ser	Leu	Val
			340					345					350		
Asp	Arg	Leu	Met	Leu	Asn	Asp	Ser	Lys	Leu	Trp	Lys	Gly	Ala	Arg	Ser
		355					360					365			

Val	Tyr	His	Gln	Leu	Phe	Met	Ser	Ser	Leu	Leu	Met	Asp	Leu	Lys	Tyr
370						375					380				
Lys	Lys	Leu	Phe	Ala	Leu	Arg	Phe	Ala	Lys	Asn	Tyr	Arg	Gln	Leu	Gln
385					390					395					400
Arg	Asp	Phe	Met	Glu	Asp	Asp	His	Glu	Arg	Ala	Val	Ser	Val	Thr	Ala
				405					410					415	
Leu	Ser	Val	Gln	Phe	Phe	Thr	Ala	Pro	Thr	Leu	Ala	Arg	Met	Leu	Leu
			420					425					430		
Thr	Glu	Glu	Asn	Leu	Met	Thr	Val	Ile	Ile	Lys	Ala	Phe	Met	Asp	His
		435					440					445			
Leu	Lys	His	Arg	Asp	Ala	Gln	Gly	Arg	Phe	Gln	Phe	Glu	Arg	Tyr	Thr
	450					455					460				
Ala	Leu	Gln	Ala	Phe	Lys	Phe	Arg	Arg	Val	Gln	Ser	Leu	Ile	Leu	Asp
465					470					475					480
Leu	Lys	Tyr	Val	Leu	Ile	Ser	Lys	Pro	Thr	Glu	Trp	Ser	Asp	Glu	Leu
				485					490					495	
Arg	Gln	Lys	Phe	Leu	Gln	Gly	Phe	Asp	Ala	Phe	Leu	Glu	Leu	Leu	Lys
			500					505					510		
Cys	Met	Gln	Gly	Met	Asp	Pro	Ile	Thr	Arg	Gln	Val	Gly	Gln	His	Ile
		515					520					525			
Glu	Met	Glu	Pro	Glu	Trp	Glu	Ala	Ala	Phe	Thr	Leu	Gln	Met	Lys	Leu
	530					535					540				
Thr	His	Val	Ile	Ser	Met	Val	Gln	Asp	Trp	Cys	Ala	Leu	Asp	Glu	Lys
545					550					555					560
Val	Leu	Ile	Glu	Ala	Tyr	Lys	Lys	Cys	Leu	Ala	Val	Leu	Thr	Gln	Cys
				565					570					575	
His	Gly	Gly	Phe	Thr	Asp	Gly	Glu	Gln	Pro	Ile	Thr	Leu	Ser	Ile	Cys
			580					585					590		
Gly	His	Ser	Val	Glu	Thr	Ile	Arg	Tyr	Cys	Val	Ser	Gln	Glu	Lys	Val
		595					600					605			
Ser	Ile	His	Leu	Pro	Ile	Ser	Arg	Leu	Leu	Ala	Gly	Leu	His	Val	Leu
	610					615					620				
Leu	Ser	Lys	Ser	Glu	Val	Ala	Tyr	Lys	Phe	Pro	Glu	Leu	Leu	Pro	Leu
625					630					635					640
Ser	Glu	Leu	Ser	Pro	Pro	Met	Leu	Ile	Glu	His	Pro	Leu	Arg	Cys	Leu
				645					650					655	
Val	Leu	Cys	Ala	Gln	Val	His	Ala	Gly	Met	Trp	Arg	Arg	Asn	Gly	Phe
			660					665					670		
Ser	Leu	Val	Asn	Gln	Ile	Tyr	Tyr	Tyr	His	Asn	Val	Lys	Cys	Arg	Arg
		675					680					685			
Glu	Met	Phe	Asp	Lys	Asp	Ile	Val	Met	Leu	Gln	Thr	Gly	Val	Ser	Met
	690					695					700				

Met	Asp	Pro	Asn	His	Phe	Leu	Met	Ile	Met	Leu	Ser	Arg	Phe	Glu	Leu
705					710					715					720
Tyr	Gln	Leu	Phe	Ser	Thr	Pro	Asp	Tyr	Gly	Lys	Arg	Phe	Ser	Ser	Glu
				725					730					735	
Val	Thr	His	Lys	Asp	Val	Val	Gln	Gln	Asn	Asn	Thr	Leu	Ile	Glu	Glu
			740					745					750		
Met	Leu	Tyr	Leu	Ile	Ile	Met	Leu	Val	Gly	Glu	Arg	Phe	Asn	Pro	Gly
		755					760					765			
Val	Gly	Gln	Val	Ala	Ala	Thr	Asp	Glu	Ile	Lys	Arg	Glu	Ile	Ile	His
	770					775					780				
Gln	Leu	Ser	Ile	Lys	Pro	Met	Ala	His	Ser	Glu	Leu	Val	Lys	Ser	Leu
785					790					795					800
Pro	Glu	Asp	Glu	Asn	Lys	Glu	Thr	Gly	Met	Glu	Ser	Val	Ile	Glu	Ser
				805					810					815	
Val	Ala	His	Phe	Lys	Lys	Pro	Gly	Leu	Thr	Gly	Arg	Gly	Met	Tyr	Glu
			820					825					830		
Leu	Lys	Pro	Glu	Cys	Ala	Lys	Glu	Phe	Asn	Leu	Tyr	Phe	Tyr	His	Phe
		835					840					845			
Ser	Arg	Ala	Glu	Gln	Ser	Lys	Ala	Glu	Glu	Ala	Gln	Arg	Lys	Leu	Lys
	850					855					860				
Arg	Glu	Asn	Lys	Glu	Asp	Thr	Ala	Leu	Pro	Pro	Pro	Ala	Leu	Pro	Pro
865					870					875					880
Phe	Cys	Pro	Leu	Phe	Ala	Ser	Leu	Val	Asn	Ile	Leu	Gln	Cys	Asp	Val
				885					890					895	
Met	Leu	Tyr	Ile	Met	Gly	Thr	Ile	Leu	Gln	Trp	Ala	Val	Glu	His	His
			900					905					910		
Gly	Ser	Ala	Trp	Ser	Glu	Ser	Met	Leu	Gln	Arg	Val	Leu	His	Leu	Ile
		915					920					925			
Gly	Met	Ala	Leu	Gln	Glu	Glu	Lys	His	His	Leu	Glu	Asn	Ala	Val	Glu
	930					935					940				
Gly	His	Val	Gln	Thr	Phe	Thr	Phe	Thr	Gln	Lys	Ile	Ser	Lys	Pro	Gly
945					950					955					960
Asp	Ala	Pro	His	Asn	Ser	Pro	Ser	Ile	Leu	Ala	Met	Leu	Glu	Thr	Leu
				965					970					975	
Gln	Asn	Ala	Pro	Ser	Leu	Glu	Ala	His	Lys	Asp	Met	Ile	Arg	Trp	Leu
		980						985					990		
Leu	Lys	Met	Phe	Asn	Ala	Ile	Lys	Lys	Ile	Arg	Glu	Cys	Ser	Ser	Ser
		995					1000					1005			
Ser	Pro	Val	Ala	Glu	Ala	Glu	Gly	Thr	Ile	Met	Glu	Glu	Ser	Ser	Arg
	1010					1015				1020					
Asp	Lys	Asp	Lys	Ala	Glu	Arg	Lys	Arg	Lys	Ala	Glu	Ile	Ala	Arg	Leu
025				1030						1035					1040

Arg Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe
1045 1050 1055

Ile Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Thr
1060 1065 1070

Ser Ala Ser Ala Thr Leu Asp Ser Ser Pro Pro Val Ser Asp Ala Ala
1075 1080 1085

Leu Thr Ala Leu Gly Pro Ala Gln Thr Gln Val Pro Glu Pro Arg Gln
1090 1095 1100

Phe Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Thr Val Gly
1105 1110 1115 1120

Ser Arg Ala Met Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu
1125 1130 1135

Ser Lys Asp Arg Thr Lys Thr Ile Ala Asp Pro Glu Lys Tyr Asp Pro
1140 1145 1150

Leu Phe Met His Pro Asp Leu Ser Cys Gly Thr His Thr Gly Ser Cys
1155 1160 1165

Gly His Val Met His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val
1170 1175 1180

Gln Ala Lys Glu Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser
1185 1190 1195 1200

Tyr Asp Val Glu Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu
1205 1210 1215

Ser Asn Thr Val Ile Pro Leu Leu Leu Pro Pro Arg Ser Ile Leu Ser
1220 1225 1230

Arg Arg Leu Asn Phe Ser Asp Gln Pro Asp Leu Ala Gln Trp Thr Arg
1235 1240 1245

Ala Val Thr Gln Gln Ile Lys Val Val Gln Met Leu Arg Arg Lys His
1250 1255 1260

Asn Ala Ala Asp Thr Ser Ser Ser Glu Asp Thr Glu Ala Met Asn Ile
1265 1270 1275 1280

Ile Pro Ile Pro Glu Gly Phe Arg Pro Asp Phe Tyr Pro Arg Asn Pro
1285 1290 1295

Tyr Ser Asp Ser Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Ala
1300 1305 1310

Tyr Lys Val Gly Leu Lys Val His Pro Asn Glu Gly Asp Pro Arg Val
1315 1320 1325

Pro Ile Leu Cys Trp Gly Thr Cys Ala Tyr Thr Ile Gln Ser Ile Glu
1330 1335 1340

Arg Ile Leu Ser Asp Glu Glu Lys Pro Val Phe Gly Pro Leu Pro Cys
1345 1350 1355 1360

Arg Leu Asp Asp Cys Leu Arg Ser Leu Thr Arg Phe Ala Ala Ala His
1365 1370 1375

Trp	Thr	Val	Ala	Leu	Leu	Pro	Val	Val	Gln	Gly	His	Phe	Cys	Lys	Leu	1380	1385	1390	
Phe	Ala	Ser	Leu	Val	Pro	Ser	Asp	Ser	Tyr	Glu	Asp	Leu	Pro	Cys	Ile	1395	1400	1405	
Leu	Asp	Ile	Asp	Met	Phe	His	Leu	Leu	Val	Gly	Leu	Val	Leu	Ala	Phe	1410	1415	1420	
Pro	Ala	Leu	Gln	Cys	Gln	Asp	Phe	Ser	Gly	Ser	Ser	Leu	Ala	Thr	Gly	425	1430	1435	1440
Asp	Leu	His	Ile	Phe	His	Leu	Val	Thr	Met	Ala	His	Ile	Val	Gln	Ile	1445	1450	1455	
Leu	Leu	Thr	Ser	Cys	Thr	Glu	Glu	Asn	Gly	Met	Asp	Gln	Glu	Asn	Pro	1460	1465	1470	
Thr	Gly	Glu	Glu	Glu	Leu	Ala	Ile	Leu	Ser	Leu	His	Lys	Thr	Leu	His	1475	1480	1485	
Gln	Tyr	Thr	Gly	Ser	Ala	Leu	Lys	Glu	Ala	Pro	Ser	Gly	Trp	His	Leu	1490	1495	1500	
Trp	Arg	Ser	Val	Arg	Ala	Ala	Ile	Met	Pro	Phe	Leu	Lys	Cys	Ser	Ala	505	1510	1515	1520
Leu	Phe	Phe	His	Tyr	Leu	Asn	Gly	Val	Pro	Ala	Pro	Pro	Asp	Leu	Gln	1525	1530	1535	
Val	Ser	Gly	Thr	Ser	His	Phe	Glu	His	Leu	Cys	Asn	Tyr	Leu	Ser	Leu	1540	1545	1550	
Pro	Thr	Asn	Leu	Ile	His	Leu	Phe	Gln	Glu	Asn	Ser	Asp	Ile	Met	Asn	1555	1560	1565	
Ser	Leu	Ile	Glu	Ser	Trp	Cys	Gln	Asn	Ser	Glu	Val	Lys	Arg	Tyr	Leu	1570	1575	1580	
Asn	Gly	Glu	Arg	Gly	Ala	Ile	Ser	Tyr	Pro	Arg	Gly	Ala	Asn	Lys	Leu	585	1590	1595	1600
Ile	Asp	Leu	Pro	Glu	Asp	Tyr	Ser	Ser	Leu	Ile	Asn	Gln	Ala	Ser	Asn	1605	1610	1615	
Phe	Ser	Cys	Pro	Lys	Ser	Gly	Gly	Asp	Lys	Ser	Arg	Ala	Pro	Thr	Leu	1620	1625	1630	
Cys	Leu	Val	Cys	Gly	Ser	Leu	Leu	Cys	Ser	Gln	Ser	Tyr	Cys	Cys	Gln	1635	1640	1645	
Ala	Glu	Leu	Glu	Gly	Glu	Asp	Val	Gly	Ala	Cys	Thr	Ala	His	Thr	Tyr	1650	1655	1660	
Ser	Cys	Gly	Ser	Gly	Ala	Gly	Ile	Phe	Leu	Arg	Val	Arg	Glu	Cys	Gln	665	1670	1675	1680
Val	Leu	Phe	Leu	Ala	Gly	Lys	Thr	Lys	Gly	Cys	Phe	Tyr	Ser	Pro	Pro	1685	1690	1695	
Tyr	Leu	Asp	Asp	Tyr	Gly	Glu	Thr	Asp	Gln	Gly	Leu	Arg	Arg	Gly	Asn	1700	1705	1710	

Pro Leu His Leu Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp
1715 1720 1725

Gln Gln His Ser Ile Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn
1730 1735 1740

Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu
745 1750 1755

<210> 7

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
-2282-91

<400> 7

ctgctcgagt ctgctcaaa c

21

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer -
2385-35

<400> 8

tctcgatatg ttgcagcctt gcta

24

<210> 9

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2282-94

<400> 9

gtatgaactt gccgaggctt tta

23

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2294-37

<400> 10

caatactttc ccagccctca gaa

23

<210> 11

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2380-88

<400> 11

atggcgctgc tagagcca

18

<210> 12

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2378-32

<400> 12

caaagcggct gagcatgac atc

23

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2381-48

<400> 13

tgaacagcca atcacactaa gca

23

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2385-94

<400> 14

ttataaatgc caaatgccaa

20

<210> 15

<211> 1757

<212> PRT

<213> Mouse

<400> 15

Met Ala Asp Glu Glu Met Asp Gly Ala Glu Arg Met Asp Val Ser Pro
1 5 10 15

Glu Pro Pro Leu Ala Pro Gln Arg Pro Ala Ser Trp Trp Asp Gln Gln
20 25 30

Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Gln Leu Val Pro
35 40 45

Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu
50 55 60

Ser	Val	Gln	Met	Ser	Ile	Leu	Thr	Pro	Leu	Glu	Trp	Tyr	Leu	Phe	Gly	65	70	75	80
Glu	Asp	Pro	Asp	Ile	Cys	Leu	Glu	Lys	Leu	Lys	His	Ser	Gly	Ala	Phe	85	90	95	
Gln	Leu	Cys	Gly	Lys	Val	Phe	Lys	Ser	Gly	Glu	Thr	Thr	Tyr	Ser	Cys	100	105	110	
Arg	Asp	Cys	Ala	Ile	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Asp	Cys	Phe	115	120	125	
Gln	Ser	Ser	Val	His	Lys	Asn	His	Arg	Tyr	Lys	Met	His	Thr	Ser	Thr	130	135	140	
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Thr	Gly	145	150	155	160
Pro	Phe	Cys	Val	Asp	His	Glu	Pro	Gly	Arg	Ala	Gly	Thr	Thr	Lys	Glu	165	170	175	
Ser	Leu	His	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	Ala	Gln	Ala	Arg	Arg	180	185	190	
Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Ile	Val	Glu	Met	Thr	Ile	Trp	Glu	195	200	205	
Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu	210	215	220	
Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His	225	230	235	240
Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala	245	250	255	
Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys	260	265	270	
Ala	Gly	Val	Tyr	Ala	Thr	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser	275	280	285	
His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His	290	295	300	
Ser	Val	Val	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp	305	310	315	320
Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys	325	330	335	
Gln	Ala	Cys	Leu	Val	Glu	Glu	Pro	Gly	Ser	Glu	Asn	Pro	Cys	Leu	Ile	340	345	350	
Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	355	360	365	
Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	370	375	380	
Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	385	390	395	400

Lys	Glu	Tyr	Ile	Ser 405	Asp	Asp	His	Glu	Arg 410	Ser	Ile	Ser	Ile	Thr	Ala 415
Leu	Ser	Val	Gln 420	Met	Leu	Thr	Val	Pro 425	Thr	Leu	Ala	Arg	His 430	Leu	Ile
Glu	Glu	Gln 435	Asn	Val	Ile	Ser	Val 440	Ile	Thr	Glu	Thr	Leu	Leu 445	Glu	Val
Leu	Pro 450	Glu	Tyr	Leu	Asp	Arg 455	Asn	Asn	Lys	Phe	Asn 460	Phe	Gln	Gly	Tyr
Ser 465	Gln	Asp	Lys	Leu	Gly 470	Arg	Val	Tyr	Ala	Val 475	Ile	Cys	Asp	Leu	Lys 480
Tyr	Ile	Leu	Ile	Ser 485	Lys	Pro	Val	Ile	Trp 490	Thr	Glu	Arg	Leu	Arg 495	Ala
Gln	Phe	Leu	Glu 500	Gly	Phe	Arg	Ser	Phe 505	Leu	Lys	Ile	Leu	Thr 510	Cys	Met
Gln	Gly	Met 515	Glu	Glu	Ile	Arg	Arg 520	Gln	Val	Gly	Gln	His 525	Ile	Glu	Val
Asp	Pro 530	Asp	Trp	Glu	Ala	Ala 535	Ile	Ala	Ile	Gln	Met 540	Gln	Leu	Lys	Asn
Ile 545	Leu	Leu	Met	Phe	Gln 550	Glu	Trp	Cys	Ala	Cys 555	Asp	Glu	Asp	Leu	Leu 560
Leu	Val	Ala	Tyr	Lys 565	Glu	Cys	His	Lys	Ala 570	Val	Met	Arg	Cys	Ser 575	Thr
Asn	Phe	Met	Ser 580	Ser	Thr	Lys	Thr	Val 585	Val	Gln	Leu	Cys	Gly 590	His	Ser
Leu	Glu	Thr 595	Lys	Ser	Tyr	Lys	Val 600	Ser	Glu	Asp	Leu	Val 605	Ser	Ile	His
Leu	Pro 610	Leu	Ser	Arg	Thr	Leu 615	Ala	Gly	Leu	His	Val 620	Arg	Leu	Ser	Arg
Leu 625	Gly	Ala	Ile	Ser	Arg 630	Leu	His	Glu	Phe	Val 635	Pro	Phe	Asp	Ser	Phe 640
Gln	Val	Glu	Val	Leu 645	Val	Glu	Tyr	Pro	Leu 650	Arg	Cys	Leu	Val	Leu 655	Val
Ala	Gln	Val 660	Val	Ala	Glu	Met	Trp	Arg 665	Arg	Asn	Gly	Leu	Ser 670	Leu	Ile
Ser	Gln	Val 675	Phe	Tyr	Tyr	Gln	Asp 680	Val	Lys	Cys	Arg	Glu 685	Glu	Met	Tyr
Asp	Lys 690	Asp	Ile	Ile	Met	Leu 695	Gln	Ile	Gly	Ala	Ser 700	Ile	Met	Asp	Pro
Asn 705	Lys	Phe	Leu	Leu	Leu 710	Val	Leu	Gln	Arg	Tyr 715	Glu	Leu	Thr	Asp	Ala 720
Phe	Asn	Lys	Thr	Ile 725	Ser	Thr	Lys	Asp	Gln 730	Asp	Leu	Ile	Lys	Gln 735	Tyr

Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	Ile	Tyr	Ile	Val	Gly
			740					745					750		
Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr	Arg	Glu	Glu	Val	Ile
		755					760					765			
Met	Arg	Glu	Ile	Thr	His	Leu	Leu	Cys	Ile	Glu	Pro	Met	Pro	His	Ser
	770					775					780				
Ala	Ile	Ala	Arg	Asn	Leu	Pro	Glu	Asn	Glu	Asn	Asn	Glu	Thr	Gly	Leu
785					790					795					800
Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys	Lys	Pro	Gly	Val	Ser
				805					810					815	
Gly	His	Gly	Val	Tyr	Glu	Leu	Lys	Asp	Glu	Ser	Leu	Lys	Asp	Phe	Asn
			820					825					830		
Met	Tyr	Phe	Tyr	His	Tyr	Ser	Lys	Thr	Gln	His	Ser	Lys	Ala	Glu	His
		835					840					845			
Met	Gln	Lys	Lys	Arg	Arg	Lys	Gln	Glu	Asn	Lys	Asp	Glu	Ala	Leu	Pro
	850					855					860				
Pro	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	Ser	Lys	Val	Val	Asn
865					870					875					880
Leu	Leu	Ser	Cys	Asp	Val	Met	Ile	Tyr	Ile	Leu	Arg	Thr	Ile	Phe	Glu
				885					890					895	
Arg	Ala	Val	Asp	Thr	Glu	Ser	Asn	Leu	Trp	Thr	Glu	Gly	Met	Leu	Gln
			900					905					910		
Met	Ala	Phe	His	Ile	Leu	Ala	Leu	Gly	Leu	Leu	Glu	Glu	Lys	Gln	Gln
		915					920					925			
Leu	Gln	Lys	Ala	Pro	Glu	Glu	Glu	Val	Ala	Phe	Asp	Phe	Tyr	His	Lys
	930					935					940				
Ala	Ser	Arg	Leu	Gly	Ser	Ser	Ala	Met	Asn	Ala	Gln	Asn	Ile	Gln	Met
945					950					955					960
Leu	Leu	Glu	Arg	Leu	Lys	Gly	Ile	Pro	Gln	Leu	Glu	Gly	Gln	Lys	Asp
				965					970					975	
Met	Ile	Thr	Trp	Ile	Leu	Gln	Met	Phe	Asp	Thr	Val	Lys	Arg	Leu	Arg
			980					985					990		
Glu	Lys	Ser	Cys	Leu	Val	Val	Ala	Thr	Thr	Ser	Gly	Leu	Glu	Cys	Ile
		995					1000					1005			
Lys	Ser	Glu	Glu	Ile	Thr	His	Asp	Lys	Glu	Lys	Ala	Glu	Arg	Lys	Arg
1010						1015					1020				
Lys	Ala	Glu	Ala	Ala	Arg	Leu	His	Arg	Gln	Lys	Ile	Met	Ala	Gln	Met
1025					1030					1035					1040
Ser	Ala	Leu	Gln	Lys	Asn	Phe	Ile	Glu	Thr	His	Lys	Leu	Met	Tyr	Asp
			1045						1050					1055	
Asn	Thr	Ser	Glu	Val	Thr	Gly	Lys	Glu	Asp	Ser	Ile	Met	Glu	Glu	Glu
			1060					1065					1070		

Ser Thr Ser Ala Val Ser Glu Ala Ser Arg Ile Ala Leu Gly Pro Lys
1075 1080 1085

Arg Gly Pro Ala Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys
1090 1095 1100

Gln Glu Glu Gln Glu Val Lys Leu Glu Asn Asn Ala Met Val Leu Ser
1105 1110 1115 1120

Ala Cys Val Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly Lys Pro
1125 1130 1135

Val Asp His Leu Gly Glu Thr Leu Asp Pro Leu Phe Met Asp Pro Asp
1140 1145 1150

Leu Ala His Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met His Ala
1155 1160 1165

Val Cys Trp Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser Gln Gln
1170 1175 1180

Arg Ile His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr Leu Cys
1185 1190 1195 1200

Pro Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile Pro Leu
1205 1210 1215

Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Glu Ala Leu Ala Gln Leu
1220 1225 1230

Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile Ser Gly
1235 1240 1245

Tyr Asn Ile Lys His Ala Lys Gly Glu Ala Pro Ala Val Pro Val Leu
1250 1255 1260

Phe Asn Gln Gly Met Gly Asp Ser Thr Phe Glu Phe His Ser Ile Leu
1265 1270 1275 1280

Ser Phe Gly Val Gln Ser Ser Val Lys Tyr Ser Asn Ser Ile Lys Glu
1285 1290 1295

Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys Val
1300 1305 1310

Pro Pro Asp Glu Leu Asp Pro Arg Val Pro Met Met Thr Trp Ser Thr
1315 1320 1325

Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu Gly
1330 1335 1340

Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Ser Gly Leu Lys
1345 1350 1355 1360

Ala Leu Met Gln Phe Ala Val Ala Gln Arg Ala Thr Cys Pro Gln Val
1365 1370 1375

Leu Ile His Lys His Leu Ala Arg Leu Leu Ser Val Ile Leu Pro Asn
1380 1385 1390

Leu Gln Ser Glu Asn Thr Pro Gly Leu Leu Ser Val Asp Leu Phe His
1395 1400 1405

Val Leu Val Gly Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp Asp
1410 1415 1420

Thr Val Asp Leu Gln Pro Ser Pro Leu Ser Ser Ser Tyr Asn His Leu
1425 1430 1435 1440

Tyr Leu Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu
1445 1450 1455

Thr Thr Asp Thr Asp Leu Ser Pro Gly Pro Pro Leu Ala Glu Gly Glu
1460 1465 1470

Glu Asp Ser Glu Glu Ala Arg Cys Ala Ser Ala Phe Phe Val Glu Val
1475 1480 1485

Ser Gln His Thr Asp Gly Leu Thr Gly Cys Gly Ala Pro Gly Trp Tyr
1490 1495 1500

Leu Trp Leu Ser Leu Arg Asn Gly Ile Thr Pro Tyr Leu Arg Cys Ala
1505 1510 1515 1520

Ala Leu Leu Phe His Tyr Leu Leu Gly Val Ala Pro Pro Glu Glu Leu
1525 1530 1535

Phe Ala Asn Ser Ala Glu Gly Glu Phe Ser Ala Leu Cys Ser Tyr Leu
1540 1545 1550

Ser Leu Pro Thr Asn Leu Phe Leu Leu Phe Gln Glu Tyr Trp Asp Thr
1555 1560 1565

Ile Arg Pro Leu Leu Gln Arg Trp Cys Gly Asp Pro Ala Leu Leu Lys
1570 1575 1580

Ser Leu Lys Gln Lys Ser Ala Val Val Arg Tyr Pro Arg Lys Arg Asn
1585 1590 1595 1600

Ser Leu Ile Glu Leu Pro Glu Asp Tyr Ser Cys Leu Leu Asn Gln Ala
1605 1610 1615

Ser His Phe Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro
1620 1625 1630

Val Leu Cys Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln Asn Ile Cys
1635 1640 1645

Cys Gln Glu Ile Val Asn Gly Glu Glu Val Gly Ala Cys Val Phe His
1650 1655 1660

Ala Leu His Cys Gly Ala Gly Val Cys Ile Phe Leu Lys Ile Arg Glu
1665 1670 1675 1680

Cys Arg Val Val Leu Val Glu Gly Lys Ala Arg Gly Cys Ala Tyr Pro
1685 1690 1695

Ala Pro Tyr Leu Asp Glu Tyr Gly Glu Thr Asp Pro Gly Leu Lys Arg
1700 1705 1710

Gly Asn Pro Leu His Leu Ser Arg Glu Arg Tyr Arg Lys Leu His Leu
1715 1720 1725

Val Trp Gln Gln His Cys Ile Ile Glu Glu Ile Ala Arg Ser Gln Glu
1730 1735 1740

1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740

Thr Asn Gln Met Leu Phe Gly Phe Asn Trp Gln Leu Leu
1745 1750 1755

<210> 16
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 16
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 17
Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10 15

<210> 18
<211> 5205
<212> DNA
<213> Homo sapiens

<400> 18
atggcggacg aggaggctgg aggtactgag aggatggaaa tcagcgcgga gttaccccag 60
accctcagc gtctggcatc ttggtgggat cagcaagttg atttttatac tgctttcttg 120
catcatttgg cacaattggt gccagaaatt tactttgctg aaatggaccc agacttggaa 180
aagcaggagg aaagtgtaca aatgtcaata ttactccac tggaatggta cttatttggg 240
gaagatccag atatttgctt agagaaattg aagcacagtg gagcatttca gctttgtggg 300
agggttttca aaagtggaga gacaacctat tcttgcaggg attgtgcaat tgatccaaca 360
tgtgtactct gtatggactg cttccaggac agtgttcata aaaatcatcg ttacaagatg 420
catacttcta ctggaggagg gttctgtgac tgtggagaca cagagggcatg gaaaactggc 480
cctttttgtg taaatcatga acctggaaga gcaggtacta taaaagagaa ttcacgctgt 540
ccgttgaatg aagaggtaat tgtccaagcc aggaaaatat ttccttcagt gataaaatat 600
gtcgtagaaa tgactatatg ggaagaggaa aaagaactgc ctctgaact ccagataagg 660
knryycvndh hsydhgtcat atacagccta caaagagctc ttgactgtga gctcgcagag 720
gccagttgc ataccactgc cattgacaaa gagggtcgtc gggctgttaa agcgggagct 780
tatgctgctt gccaggaagc aaaggaagat ataaagagtc attcagaaaa tgtctctcaa 840

catccacttc atgtagaagt attacactca gagattatgg ctcatcagaa atttgctttg 900
cgtcttggtt cctggatgaa caaaattatg agctattcaa gtgacttttag gcagatcttt 960
tgccaagcat gccttagaga agaacctgac tcggagaatc cctgtctcat aagcagggtta 1020
atgctttggg atgcaaagct ttataaagggt gcccgtaaga tccttcatga attgatcttc 1080
agcagttttt ttatggagat ggaatacaaa aaactctttg ctatggaatt tgtgaagtat 1140
tataaacaac tgcagaaaga atatatcagt gatgatcatg acagaagtat ctctataact 1200
gcactttcag ttcagatggt tactgttcct actctggctc gacatcttat tgaagagcag 1260
aatgttatct ctgtcattac tgaaactctg ctagaagttt tacctgagta cttggacagg 1320
aacaataaat tcaacttcca gggttatagc caggacaaat tgggaagagt atatgcagta 1380
atatgtgacc taaagtatat cctgatcagc aaaccacaa tatggacaga aagattaaga 1440
atgcagttcc ttgaagggtt tcgatctttt ttgaagattc ttacctgtat gcagggaatg 1500
gaagaaatcc gaagacagggt tgggcaacac attgaagtgg atcctgattg ggaggctgcc 1560
attgctatac agatgcaatt gaagaatatt ttactcatgt tccaagagtg gtgtgcttgt 1620
gatgaagaac tcttacttgt ggcttataaa gaatgtcaca aagctgtgat gaggtgcagt 1680
accagtttca tatctagtag caagacagta gtacaatcgt gtggacatag tttggaaaca 1740
aagtcctaca gagtatctga ggatcttgta agcatacatc tgccactctc taggaccctt 1800
gctggtcttc atgtacgttt aagcaggctg ggtgctgttt caagactgca tgaatttgtg 1860
tcttttgagg actttcaagt agaggtaacta gtggaatatc ctttacgttg tctggtgttg 1920
gttgcccagg ttgttgctga gatgtggcga agaaatggac tgtctcttat tagccagggtg 1980
ttttattacc aagatgttaa gtgcagagaa gaaatgtatg ataaagatat catcatgctt 2040
cagattggtg catctttaat ggatcccaat aagttcttgt tactggtact tcagaggtat 2100
gaacttgccg aggcttttaa caagaccata tctacaaaag accaggattt gattaaacaa 2160
tataatacac taatagaaga aatgcttcag gtcctcatct atattgtggg tgagcgttat 2220
gtacctggag tgggaaatgt gaccaaagaa gaggtcacao tgagagaaat cattcacttg 2280
ctttgcattg aacctatgcc acacagtgcc attgccaaaa atttacctga gaatgaaaat 2340
aatgaaactg gcttagagaa tgtcataaac aaagtggcca catttaagaa accagggtgta 2400
tcaggccatg gagtttatga actaaaagat gaatcactga aagacttcaa tatgtacttt 2460
tatcattact ccaaaccaca gcatagcaag gctgaacata tgcagaagaa aaggagaaaa 2520
caagaaaaa aagatgaagc attgccgcca ccaccacctc ctgaattctg ccctgctttc 2580
agcaaagtga ttaaccttct caactgtgat atcatgatgt acattctcag gaccgtattt 2640
gagcgggcaa tagacacaga ttctaacttg tggaccgaag ggatgctcca aatggctttt 2700
catattctgg cattgggttt actagaagag aagcaacagc ttcaaaaagc tcctgaagaa 2760

gaagtaacat ttgactttta tcataaggct tcaagattgg gaagttcagc catgaatata 2820
caaatgcttt tggaaaaact caaaggaatt cccagttag aaggccagaa ggacatgata 2880
acgtggatac ttcagatggt tgacacagtg aagcgattaa gagaaaaatc ttgtttaatt 2940
gtagcaacca catcaggatc ggaatctatt aagaatgatg agattactca tgataaagaa 3000
aaagcagaac gaaaaagaaa agctgaagct gctaggctac atcgccagaa gatcatggct 3060
cagatgtctg ccttacagaa aaacttcatt gaaactcata aactcatgta tgacaatata 3120
tcagaaatgc ctgggaaaga agattccatt atggaggaag agagcaccac agcagtcagt 3180
gactactcta gaattgcttt gggctcctaaa cggggctccat ctgttactga aaaggaggtg 3240
ctgacgtgca tcctttgcca agaagaacag gaggtgaaaa tagaaaataa tgccatggta 3300
ttatcggcct gtgtccagaa atctactgcc ttaaccacag acaggggaaa acccatagaa 3360
ctctcaggag aagccctaga cccacttttc atggatccag acttggcata tggaacttat 3420
acaggaagct gtggtcatgt aatgcacgca gtgtgctggc agaagtattt tgaagctgta 3480
cagctgagct ctcagcagcg cattcatggt gacctttttg acttggaag tggagaatat 3540
ctttgccctc tttgcaaate tctgtgcaat actgtgatcc ccattattcc tttgcaacct 3600
caaaagataa acagtgagaa tgcagatgct cttgctcaac ttttgacct ggcacgggtg 3660
atacagactg ttctggccag aatatcaggt tataatataa gacatgctaa aggagaaaac 3720
ccaattccta ttttctttta tcaaggaatg ggagattcta ctttggagtt ccattccatc 3780
ctgagttttg gcgttgagtc ttcgattaaa tattcaaata gcatcaagga aatgggttatt 3840
ctctttgcca caacaattta tagaattgga ttgaaagtgc cacctgatga aagggatcct 3900
cgagtcccca tgctgacctg gagcacctgc gctttcacta tccaggcaat tgaaaatcta 3960
ttgggagatg aaggaaaacc tctgtttgga gcacttcaaa ataggcagca taatgggtctg 4020
aaagcattaa tgcagtttgc agttgcacag aggattacct gtcctcaggt cctgatacag 4080
aaacatctgg ttcgtcttct atcagttggt cttcctaaca taaaatcaga agatacacca 4140
tgccttctgt ctatagatct gtttcatggt ttggtgggtg ctgtgttagc attcccatcc 4200
ttgtattggg atgacctgt tgatctgcag ccttcttcag ttagttcttc ctataaccac 4260
ctttatctct tccatttgat caccatggca cacatgcttc agatactact tacagtagac 4320
acaggcctac cccttgctca ggttcaagaa gacagtgaag aggctcattc cgcattctct 4380
ttctttgcag aaatttctca atatacaagt ggctccattg ggtgtgatat tctgggtg 4440
tatttggtgg tctcactgaa gaatggcatc accccttctc ttcgctgtgc tgcattgttt 4500
ttccactatt tacttggggg aactccgcct gaggaactgc ataccaattc tgcagaagga 4560
gagtacagt cactctgtag ctatctatct ttacctaca atttgttcct gctcttcag 4620
gaatattggg atactgtaag gcccttgctc cagagggggt gtgcagatcc tgccttacta 4680

aactgtttga agcaaaaaaa caccgtgggc aggtacccta gaaaaagaaa tagtttgata 4740
gagcttcctg atgactatag ctgcctcctg aatcaagctt ctcatttcag gtgccacagg 4800
tctgcagatg atgagcgaaa gcacccctgtc ctctgccttt tctgtggggc tatactatgt 4860
tctcagaaca tttgctgcca ggaaattgtg aacgggggaag aggttgaggc ttgcattttt 4920
cacgcacttc actgtggagc cggagtctgc attttcctaa aaatcagaga atgccgagtg 4980
gtcctgggtg aaggtaaagc cagaggctgt gcctatccag ctccttactt ggatgaatat 5040
ggagaaacag accctggcct gaagaggggc aacccccttc atttatctcg tgagcgggat 5100
cggaagctcc atttggtctg gcaacaacac tgcattatag aagagattgc taggagccaa 5160
gagactaatc agatgttatt tggattcaac tggcagttac tgtga 5205

<210> 19
<211> 1735
<212> PRT
<213> Homo sapiens

<400> 19
Ala Met Glu Gly Asn Met Ala Asp Glu Glu Ala Gly Gly Thr Glu Arg
1 5 10 15
Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser
20 25 30
Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala Phe Leu His His Leu
35 40 45
Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu
50 55 60
Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu
65 70 75 80
Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys
85 90 95
His Ser Gly Ala Phe Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu
100 105 110
Thr Thr Tyr Ser Cys Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu
115 120 125
Cys Met Asp Cys Phe Gln Asp Ser Val His Lys Asn His Arg Tyr Lys
130 135 140
Met His Thr Ser Thr Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu
145 150 155 160
Ala Trp Lys Thr Gly Pro Phe Cys Val Asn His Glu Pro Gly Arg Ala
165 170 175
Gly Thr Ile Lys Glu Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile
180 185 190
Val Gln Ala Arg Lys Ile Phe Pro Ser Val Ile Lys Tyr Val Val Glu
195 200 205

Met	Thr	Ile	Trp	Glu	Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile
210						215					220				
Arg	Glu	Lys	Asn	Glu	Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His
225					230					235					240
His	Ser	Tyr	Asp	His	Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys
				245					250					255	
Glu	Leu	Ala	Glu	Ala	Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly
			260					265					270		
Arg	Arg	Ala	Val	Lys	Ala	Gly	Ala	Tyr	Ala	Ala	Cys	Gln	Glu	Ala	Lys
		275					280					285			
Glu	Asp	Ile	Lys	Ser	His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His
	290					295					300				
Val	Glu	Val	Leu	His	Ser	Glu	Ile	Met	Ala	His	Gln	Lys	Phe	Ala	Leu
305					310					315					320
Arg	Leu	Gly	Ser	Trp	Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe
				325					330					335	
Arg	Gln	Ile	Phe	Cys	Gln	Ala	Cys	Leu	Arg	Glu	Glu	Pro	Asp	Ser	Glu
			340					345					350		
Asn	Pro	Cys	Leu	Ile	Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr
		355					360					365			
Lys	Gly	Ala	Arg	Lys	Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe
	370					375					380				
Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr
385					390					395					400
Tyr	Lys	Gln	Leu	Gln	Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Asp	Arg	Ser
				405					410					415	
Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu
			420					425					430		
Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu
		435					440					445			
Thr	Leu	Leu	Glu	Val	Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe
	450					455					460				
Asn	Phe	Gln	Gly	Tyr	Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val
465					470					475					480
Ile	Cys	Asp	Leu	Lys	Tyr	Ile	Leu	Ile	Ser	Lys	Pro	Thr	Ile	Trp	Thr
				485					490					495	
Glu	Arg	Leu	Arg	Met	Gln	Phe	Leu	Glu	Gly	Phe	Arg	Ser	Phe	Leu	Lys
				500				505					510		
Ile	Leu	Thr	Cys	Met	Gln	Gly	Met	Glu	Glu	Ile	Arg	Arg	Gln	Val	Gly
		515					520					525			
Gln	His	Ile	Glu	Val	Asp	Pro	Asp	Trp	Glu	Ala	Ala	Ile	Ala	Ile	Gln
	530					535					540				

Met	Gln	Leu	Lys	Asn	Ile	Leu	Leu	Met	Phe	Gln	Glu	Trp	Cys	Ala	Cys	
545					550					555					560	
Asp	Glu	Glu	Leu	Leu	Leu	Val	Ala	Tyr	Lys	Glu	Cys	His	Lys	Ala	Val	
			565						570					575		
Met	Arg	Cys	Ser	Thr	Ser	Phe	Ile	Ser	Ser	Ser	Lys	Thr	Val	Val	Gln	
			580					585					590			
Ser	Cys	Gly	His	Ser	Leu	Glu	Thr	Lys	Ser	Tyr	Arg	Val	Ser	Glu	Asp	
		595					600					605				
Leu	Val	Ser	Ile	His	Leu	Pro	Leu	Ser	Arg	Thr	Leu	Ala	Gly	Leu	His	
	610					615					620					
Val	Arg	Leu	Ser	Arg	Leu	Gly	Ala	Val	Ser	Arg	Leu	His	Glu	Phe	Val	
625					630					635					640	
Ser	Phe	Glu	Asp	Phe	Gln	Val	Glu	Val	Leu	Val	Glu	Tyr	Pro	Leu	Arg	
				645					650					655		
Cys	Leu	Val	Leu	Val	Ala	Gln	Val	Val	Ala	Glu	Met	Trp	Arg	Arg	Asn	
			660					665					670			
Gly	Leu	Ser	Leu	Ile	Ser	Gln	Val	Phe	Tyr	Tyr	Gln	Asp	Val	Lys	Cys	
		675					680					685				
Arg	Glu	Glu	Met	Tyr	Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala	
	690					695					700					
Ser	Leu	Met	Asp	Pro	Asn	Lys	Phe	Leu	Leu	Leu	Val	Leu	Gln	Arg	Tyr	
705					710					715					720	
Glu	Leu	Ala	Glu	Ala	Phe	Asn	Lys	Thr	Ile	Ser	Thr	Lys	Asp	Gln	Asp	
				725					730					735		
Leu	Ile	Lys	Gln	Tyr	Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	
			740					745					750			
Ile	Tyr	Ile	Val	Gly	Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr	
	755						760					765				
Lys	Glu	Glu	Val	Thr	Met	Arg	Glu	Ile	Ile	His	Leu	Leu	Cys	Ile	Glu	
	770					775					780					
Pro	Met	Pro	His	Ser	Ala	Ile	Ala	Lys	Asn	Leu	Pro	Glu	Asn	Glu	Asn	
785					790					795					800	
Asn	Glu	Thr	Gly	Leu	Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys	
				805					810					815		
Lys	Pro	Gly	Val	Ser	Gly	His	Gly	Val	Tyr	Glu	Leu	Lys	Asp	Glu	Ser	
			820					825					830			
Leu	Lys	Asp	Phe	Asn	Met	Tyr	Phe	Tyr	His	Tyr	Ser	Lys	Thr	Gln	His	
		835					840					845				
Ser	Lys	Ala	Glu	His	Met	Gln	Lys	Lys	Arg	Arg	Lys	Gln	Glu	Asn	Lys	
	850					855					860					
Asp	Glu	Ala	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	
865					870					875					880	

Ser Lys Val Ile Asn Leu Leu Asn Cys Asp Ile Met Met Tyr Ile Leu
885 890 895

Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp Ser Asn Leu Trp Thr
900 905 910

Glu Gly Met Leu Gln Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu
915 920 925

Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu Glu Glu Val Thr Phe
930 935 940

Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ile
945 950 955 960

Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln
965 970 975

Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg
980 985 990

Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu
995 1000 1005

Ser Ile Lys Asn Asp Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg
1010 1015 1020

Lys Arg Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala
1025 1030 1035 1040

Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met
1045 1050 1055

Tyr Asp Asn Thr Ser Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu
1060 1065 1070

Glu Glu Ser Thr Pro Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly
1075 1080 1085

Pro Lys Arg Gly Pro Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile
1090 1095 1100

Leu Cys Gln Glu Glu Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val
1105 1110 1115 1120

Leu Ser Ala Cys Val Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly
1125 1130 1135

Lys Pro Ile Glu Leu Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp
1140 1145 1150

Pro Asp Leu Ala Tyr Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met
1155 1160 1165

His Ala Val Cys Trp Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser
1170 1175 1180

Gln Gln Arg Ile His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr
1185 1190 1195 1200

Leu Cys Pro Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile
1205 1210 1215

Pro Leu Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala
1220 1225 1230

Gln Leu Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile
1235 1240 1245

Ser Gly Tyr Asn Ile Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile
1250 1255 1260

Phe Phe Asn Gln Gly Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile
1265 1270 1275 1280

Leu Ser Phe Gly Val Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys
1285 1290 1295

Glu Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys
1300 1305 1310

Val Pro Pro Asp Glu Arg Asp Pro Arg Val Pro Met Leu Thr Trp Ser
1315 1320 1325

Thr Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu
1330 1335 1340

Gly Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Asn Gly Leu
1345 1350 1355 1360

Lys Ala Leu Met Gln Phe Ala Val Ala Gln Arg Ile Thr Cys Pro Gln
1365 1370 1375

Val Leu Ile Gln Lys His Leu Val Arg Leu Leu Ser Val Val Leu Pro
1380 1385 1390

Asn Ile Lys Ser Glu Asp Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe
1395 1400 1405

His Val Leu Val Gly Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp
1410 1415 1420

Asp Pro Val Asp Leu Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His
1425 1430 1435 1440

Leu Tyr Leu Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu
1445 1450 1455

Leu Thr Val Asp Thr Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser
1460 1465 1470

Glu Glu Ala His Ser Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr
1475 1480 1485

Thr Ser Gly Ser Ile Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp Val
1490 1495 1500

Ser Leu Lys Asn Gly Ile Thr Pro Tyr Leu Arg Cys Ala Ala Leu Phe
1505 1510 1515 1520

Phe His Tyr Leu Leu Gly Val Thr Pro Pro Glu Glu Leu His Thr Asn
1525 1530 1535

Ser Ala Glu Gly Glu Tyr Ser Ala Leu Cys Ser Tyr Leu Ser Leu Pro
1540 1545 1550

Thr Asn Leu Phe Leu Leu Phe Gln Glu Tyr Trp Asp Thr Val Arg Pro
1555 1560 1565

Leu Leu Gln Arg Arg Cys Ala Asp Pro Ala Leu Leu Asn Cys Leu Lys
1570 1575 1580

Gln Lys Asn Thr Val Val Arg Tyr Pro Arg Lys Arg Asn Ser Leu Ile
1585 1590 1595 1600

Glu Leu Pro Asp Asp Tyr Ser Cys Leu Leu Asn Gln Ala Ser His Phe
1605 1610 1615

Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro Val Leu Cys
1620 1625 1630

Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln Asn Ile Cys Cys Gln Glu
1635 1640 1645

Ile Val Asn Gly Glu Glu Val Gly Ala Cys Ile Phe His Ala Leu His
1650 1655 1660

Cys Lys Ala Arg Gly Cys Ala Tyr Pro Ala Pro Tyr Leu Asp Glu Tyr
1665 1670 1675 1680

Gly Glu Thr Asp Pro Gly Leu Lys Arg Gly Asn Pro Leu His Leu Ser
1685 1690 1695

Arg Glu Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile
1700 1705 1710

Ile Glu Glu Ile Ala Arg Ser Gln Glu Thr Asn Gln Met Leu Phe Gly
1715 1720 1725

Phe Asn Trp Gln Leu Leu *
1730 1735

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 20
agaaggagag tacagtgcac tc

22

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 21
cgaaagcatc ctgtcctctg

20

<210> 22
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 22
aggaagctgt ggtcatgt 18

<210> 23
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 23
gttaggaaga actg 14

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 24
aagaacagcg aaggcaacag 20

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 25
cgcagctacc ccaacacatt ct 22

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 26
tttcttccat tccctgcata ca 22

<210> 27
<211> 25
<212> DNA
<213> Artificial Sequence

<223> Description of Artificial Sequence: PCR Primer

25

<220>
<223> Description of Artificial Sequence: PCR Primer

23

<220>
<223> Description of Artificial Sequence: PCR Primer

21

11-11-68 11-11-68 11-11-68 11-11-68 11-11-68